

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: July 1, 2003, 10:33:36 ; Search time 73 Seconds
(without alignments)
1084.258 Million cell updates/sec

Title: US-10-080-233-2

Perfect score: 3189

Sequence: 1 MFKSMQLAAAGSLTGVLG.....AQEPYRDEILEDGIEE 594

Scoring table:

BLOSUM62
Gapop 10.0, Gapext 0.5

Searched: 908470 seqs, 133250620 residues

Minimum number of hits satisfying chosen parameters: 908470

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Database :

1: /SID22/gcgdata/geneeqq-emb1/AA1980.DAT:*
2: /SID22/gcgdata/geneeqq-emb1/AA1981.DAT:*
3: /SID22/gcgdata/geneeqq-emb1/AA1982.DAT:*
4: /SID22/gcgdata/geneeqq-emb1/AA1983.DAT:*
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14: /SID22/gcgdata/geneeqq-emb1/AA1993.DAT:*
15: /SID22/gcgdata/geneeqq-emb1/AA1994.DAT:*
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17: /SID22/gcgdata/geneeqq-emb1/AA1996.DAT:*
18: /SID22/gcgdata/geneeqq-emb1/AA1997.DAT:*
19: /SID22/gcgdata/geneeqq-emb1/AA1998.DAT:*
20: /SID22/gcgdata/geneeqq-emb1/AA1999.DAT:*
21: /SID22/gcgdata/geneeqq-emb1/AA2000.DAT:*
22: /SID22/gcgdata/geneeqq-emb1/AA2001.DAT:*
23: /SID22/gcgdata/geneeqq-emb1/AA2002.DAT:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	3189	100.0	594	20	Stachybotrys chart
2	3189	100.0	594	20	Stachybotrys pheno
3	3189	100.0	594	21	Stachybotrys chart
4	3189	100.0	594	21	Stachybotrys chart
5	3189	100.0	594	23	Stachybotrys phenol
6	1954.5	61.3	627	21	Biopolaris spicifer
7	1954.5	61.3	627	21	Biopolaris spicifer
8	1954.5	61.3	627	23	Biopolaris spicifer
9	1929.5	60.5	627	21	Curvularia pallesc
10	1929.5	60.5	627	21	Curvularia pallesc

11	1929.5	60.5	627	23	AA018212	C pallescens pheno
12	1735.5	54.4	583	23	AA097312	Phenol oxidising e
13	1731.5	54.3	583	23	AA097316	Phenol oxidising e
14	1731.5	54.3	583	23	AA097318	Phenol oxidising e
15	1731.5	54.3	583	23	AA097318	Phenol oxidising e
16	1731.5	54.3	583	23	AA097318	Phenol oxidising e
17	1730.5	54.3	583	23	AA097321	Phenol oxidising e
18	1730.5	54.3	583	23	AA097324	Phenol oxidising e
19	1730.5	54.3	583	23	AA097323	Phenol oxidising e
20	1730.5	54.3	583	23	AA097323	Phenol oxidising e
21	1730.5	54.3	583	23	AA097323	Phenol oxidising e
22	1730.5	54.3	583	23	AA097329	Phenol oxidising e
23	1729.5	54.2	583	23	AA097329	Phenol oxidising e
24	1729.5	54.2	583	23	AA097334	Phenol oxidising e
25	1729.5	54.2	583	23	AA097336	Phenol oxidising e
26	1729.5	54.2	583	23	AA097336	Phenol oxidising e
27	1729.5	54.2	583	23	AA097336	Phenol oxidising e
28	1729.5	54.2	583	23	AA097336	Phenol oxidising e
29	1729.5	54.2	583	23	AA097336	Phenol oxidising e
30	1728.5	54.2	583	23	AA097333	Phenol oxidising e
31	1728.5	54.2	583	23	AA097337	Phenol oxidising e
32	1728.5	54.2	583	23	AA097338	Phenol oxidising e
33	1728.5	54.2	583	23	AA097356	Phenol oxidising e
34	1728.5	54.2	583	23	AA097356	Phenol oxidising e
35	1728.5	54.2	583	23	AA097357	Phenol oxidising e
36	1728.5	54.2	583	23	AA097357	Phenol oxidising e
37	1728.5	54.2	583	23	AA097357	Phenol oxidising e
38	1728.5	54.2	583	23	AA097357	Phenol oxidising e
39	1728.5	54.2	583	23	AA097357	Phenol oxidising e
40	1728.5	54.2	583	23	AA097357	Phenol oxidising e
41	1727.5	54.2	583	23	AA097320	Phenol oxidising e
42	1727.5	54.2	583	23	AA097326	Phenol oxidising e
43	1727.5	54.2	583	23	AA097335	Phenol oxidising e
44	1727.5	54.2	583	23	AA097335	Phenol oxidising e
45	1727.5	54.2	583	23	AA097335	Phenol oxidising e

ALIGNMENTS

RESULT 1
AA045222 standard; Protein: 594 AA.
ID AA045222:
AC AA045222:
DE 05-JAN-2000 (first entry)
XX
XX Stachybotrys chartarum phenol oxidising enzyme.
XX Stachybotrys chartarum: phenol oxidising enzyme; colour: dye;
XX detergent; anti-dye transfer; stain removal; bleaching.
XX
XX Stachybotrys chartarum.
XX
XX MO9949010-AA2.
XX
XX 30-SEP-1999.
XX
XX 23-MAR-1999; 99WO-EP02042.
XX
XX 24-MAR-1998; 98US-0046969.
XX
XX 22-DEC-1998; 98US-0218702.
XX
XX (UNITL) UNILEVER NV.
XX (UNITL) UNILEVER PLC.
XX
XX Convents D, Amory A, Wang H, Dhasee P, Lambrechts-Rongvaux A;
XX Wang C;
XX WPI, 1999-601211/51.
XX N-PSDB; AA025727.
XX

PT Detergent composition containing phenol oxidase from Stachybotrys, used
 to bleach stains and prevent dye transfer

PS Claim 16; Fig 5; 56pp; English.

CC The present invention describes a detergent composition containing a
 purified phenol oxidising enzyme derived from Stachybotrys. The present
 CC sequence represents Stachybotrys chartarum phenol oxidising enzyme. The
 CC enzyme can be used to modify the colour of dyes and other coloured
 CC compounds (e.g. for use in pulp and paper bleaching also for removing
 CC stains, e.g. food, tea, blood etc., from fabrics) and for preventing dye
 CC transfer during fabric washing.

XX Sequence 594 AA:

Query Match 100.0%; Score 3189; DB 20; Length 594;
 Best Local Similarity 100.0%; Pred. No. 2.9e-299;
 Matches 594; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 MLFKSMQLAASGLISGLVIGIPMDTGSHPREAVDEVKTEVPADSLAAGDDWESPYP 60
 1 MLFKSMQLAASGLISGLVIGIPMDTGSHPREAVDEVKTEVPADSLAAGDDWESPYP 60
 61 NLTVNALPIPVKOPKMITNPVTKDIWYEIEIKRFOQRIYPTLRPATLVGDGMS 120
 61 NLTVNALPIPVKOPKMITNPVTKDIWYEIEIKRFOQRIYPTLRPATLVGDGMS 120
 QY 121 GPTFVNPRTGTEVAFINNATVENSVHLHGSRSRAPFGMAEDVTFPEGEKDYEPNQS 180
 121 GPTFVNPRTGTEVAFINNATVENSVHLHGSRSRAPFGMAEDVTFPEGEKDYEPNQS 180
 Db 121 GPTFVNPRTGTEVAFINNATVENSVHLHGSRSRAPFGMAEDVTFPEGEKDYEPNQS 180
 QY 181 ARLMYHDHAFPKTAENAYFGQAGAYIINDEAEDALGPSYGEFDIPLIITAKYYNADG 240
 181 ARLMYHDHAFPKTAENAYFGQAGAYIINDEAEDALGPSYGEFDIPLIITAKYYNADG 240
 Db 181 ARLMYHDHAFPKTAENAYFGQAGAYIINDEAEDALGPSYGEFDIPLIITAKYYNADG 240
 QY 241 TLRSFEGDODLMGVHVNQOPMPELVNVPKRYFRFLNAVASAWLLYVRTSSPNVR 300
 241 TLRSFEGDODLMGVHVNQOPMPELVNVPKRYFRFLNAVASAWLLYVRTSSPNVR 300
 Db 241 TLRSFEGDODLMGVHVNQOPMPELVNVPKRYFRFLNAVASAWLLYVRTSSPNVR 300
 QY 301 IPFOVIASDAGILQAPVQTSNLYLAVEREYIIDFTNFAQOTLDLRNVAETNDVDEDE 360
 301 IPFOVIASDAGILQAPVQTSNLYLAVEREYIIDFTNFAQOTLDLRNVAETNDVDEDE 360
 Db 301 IPFOVIASDAGILQAPVQTSNLYLAVEREYIIDFTNFAQOTLDLRNVAETNDVDEDE 360
 QY 361 YARLEVMRFVYSSGTEVDNSQVSTLRDVPFPKKEGSPADKHFEERSNGHYLLINDVGE 420
 361 YARLEVMRFVYSSGTEVDNSQVSTLRDVPFPKKEGSPADKHFEERSNGHYLLINDVGE 420
 Db 361 YARLEVMRFVYSSGTEVDNSQVSTLRDVPFPKKEGSPADKHFEERSNGHYLLINDVGE 420
 QY 421 ADVNERVLAKPELGIVEWELENSGSGSHVPHILVDKILKRTGGGQVMPYESAGLK 480
 421 ADVNERVLAKPELGIVEWELENSGSGSHVPHILVDKILKRTGGGQVMPYESAGLK 480
 Db 421 ADVNERVLAKPELGIVEWELENSGSGSHVPHILVDKILKRTGGGQVMPYESAGLK 480
 QY 481 DVVNLGRGETLTIEAHYQPTGAYMMHCHNLIHEDNDMAAFVNTAMEEKYLOEDFEDP 540
 481 DVVNLGRGETLTIEAHYQPTGAYMMHCHNLIHEDNDMAAFVNTAMEEKYLOEDFEDP 540
 Db 481 DVVNLGRGETLTIEAHYQPTGAYMMHCHNLIHEDNDMAAFVNTAMEEKYLOEDFEDP 540
 QY 541 MNPKRAVPYRNDFHARAGNFSASITARVOELAEQEPYNRLEIDELDIGEE 594
 541 MNPKRAVPYRNDFHARAGNFSASITARVOELAEQEPYNRLEIDELDIGEE 594
 Db 541 MNPKRAVPYRNDFHARAGNFSASITARVOELAEQEPYNRLEIDELDIGEE 594

RESULT 2
 AAY39992
 ID AAY39992 standard; Protein; 594 AA.

XX AAY39992;

XX 16-DEC-1999 (first entry)

XX Stachybotrys phenol oxidase protein sequence.

XX Phenol oxidase; enzyme; coloured compound; dye transfer prevention;
 KW fabric washing; stain bleaching; anti-dye transfer; detergent.
 XX

OS Stachybotrys chartarum.

XX WO9949020-A2.

XX 30-SEP-1999.

XX 23-MAR-1999; 99WO-US06327.

XX 24-MAR-1998; 98US-0046969.

XX 22-DEC-1998; 98US-0218702.

XX 22-MAR-1999; 99US-0273957.

XX (GENV) GENENCOR INT INC.

XX Amory A, Wang H, Phase P, Lambrechts-Rongvaux A, Wang C;

XX WPT: 1999-591068/50.

XX N-PSDB: AA27601, AA27602.

XX Novel enzyme for modifying coloured compounds used to prevent
 PT dye-transfer.

XX Claim 16; Fig 5; 64pp; English.

XX This sequence is the Stachybotrys chartarum phenol oxidase enzyme
 CC of the invention. The invention is used to modify a coloured compound and
 CC prevent dye transfer during fabric washing, or for stain bleaching or
 CC anti-dye transfer. It is useful in the detergent, paper and pulp, textile
 CC and food industries.

XX Sequence 594 AA:

Query Match 100.0%; Score 3189; DB 20; Length 594;
 Best Local Similarity 100.0%; Pred. No. 2.9e-299;
 Matches 594; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 MLFKSMQLAASGLISGLVIGIPMDTGSHPREAVDEVKTEVPADSLAAGDDWESPYP 60
 1 MLFKSMQLAASGLISGLVIGIPMDTGSHPREAVDEVKTEVPADSLAAGDDWESPYP 60
 Db 1 MLFKSMQLAASGLISGLVIGIPMDTGSHPREAVDEVKTEVPADSLAAGDDWESPYP 60
 QY 61 NLTVNALPIPVKOPKMITNPVTKDIWYEIEIKRFOQRIYPTLRPATLVGDGMS 120
 61 NLTVNALPIPVKOPKMITNPVTKDIWYEIEIKRFOQRIYPTLRPATLVGDGMS 120
 Db 61 NLTVNALPIPVKOPKMITNPVTKDIWYEIEIKRFOQRIYPTLRPATLVGDGMS 120
 QY 121 GPTFVNPRTGTEVAFINNATVENSVHLHGSRSRAPFGMAEDVTFPEGEKDYEPNQS 180
 121 GPTFVNPRTGTEVAFINNATVENSVHLHGSRSRAPFGMAEDVTFPEGEKDYEPNQS 180
 Db 121 GPTFVNPRTGTEVAFINNATVENSVHLHGSRSRAPFGMAEDVTFPEGEKDYEPNQS 180
 QY 181 ARLMYHDHAFPKTAENAYFGQAGAYIINDEAEDALGPSYGEFDIPLIITAKYYNADG 240
 181 ARLMYHDHAFPKTAENAYFGQAGAYIINDEAEDALGPSYGEFDIPLIITAKYYNADG 240
 Db 181 ARLMYHDHAFPKTAENAYFGQAGAYIINDEAEDALGPSYGEFDIPLIITAKYYNADG 240
 QY 241 TLRSFEGDODLMGVHVNQOPMPELVNVPKRYFRFLNAVASAWLLYVRTSSPNVR 300
 241 TLRSFEGDODLMGVHVNQOPMPELVNVPKRYFRFLNAVASAWLLYVRTSSPNVR 300
 Db 241 TLRSFEGDODLMGVHVNQOPMPELVNVPKRYFRFLNAVASAWLLYVRTSSPNVR 300
 QY 301 IPFOVIASDAGILQAPVQTSNLYLAVEREYIIDFTNFAQOTLDLRNVAETNDVDEDE 360
 301 IPFOVIASDAGILQAPVQTSNLYLAVEREYIIDFTNFAQOTLDLRNVAETNDVDEDE 360
 Db 301 IPFOVIASDAGILQAPVQTSNLYLAVEREYIIDFTNFAQOTLDLRNVAETNDVDEDE 360
 QY 361 YARLEVMRFVYSSGTEVDNSQVSTLRDVPFPKKEGSPADKHFEERSNGHYLLINDVGE 420
 361 YARLEVMRFVYSSGTEVDNSQVSTLRDVPFPKKEGSPADKHFEERSNGHYLLINDVGE 420
 Db 361 YARLEVMRFVYSSGTEVDNSQVSTLRDVPFPKKEGSPADKHFEERSNGHYLLINDVGE 420
 QY 421 ADVNERVLAKPELGIVEWELENSGSGSHVPHILVDKILKRTGGGQVMPYESAGLK 480
 421 ADVNERVLAKPELGIVEWELENSGSGSHVPHILVDKILKRTGGGQVMPYESAGLK 480
 Db 421 ADVNERVLAKPELGIVEWELENSGSGSHVPHILVDKILKRTGGGQVMPYESAGLK 480
 QY 481 DVVNLGRGETLTIEAHYQPTGAYMMHCHNLIHEDNDMAAFVNTAMEEKYLOEDFEDP 540
 481 DVVNLGRGETLTIEAHYQPTGAYMMHCHNLIHEDNDMAAFVNTAMEEKYLOEDFEDP 540
 Db 481 DVVNLGRGETLTIEAHYQPTGAYMMHCHNLIHEDNDMAAFVNTAMEEKYLOEDFEDP 540
 QY 541 MNPKRAVPYRNDFHARAGNFSASITARVOELAEQEPYNRLEIDELDIGEE 594
 541 MNPKRAVPYRNDFHARAGNFSASITARVOELAEQEPYNRLEIDELDIGEE 594
 Db 541 MNPKRAVPYRNDFHARAGNFSASITARVOELAEQEPYNRLEIDELDIGEE 594

Db 541 MNPKRAVPYNRNDFHARAGNFSAESITARVOELAEDEPYNRLEIDEDGIEE 594

RESULT 3
AAV95537 standard; Protein: 594 AA.
ID AAV95537
AC AAV95537
DT 10-OCT-2000 (first entry)
DE Stachybotrys chartarum phenol oxidizing enzyme.
KM Phenol oxidizing enzyme; detergent; bleaching.
OS Stachybotrys chartarum.
MO200039306-A2.
06-JUL-2000.
PF 20-DEC-1999; 99WO-EPI0287.
PR 23-DEC-1998; 98US-0220871.
PR 23-JUN-1999; 99US-0338723.
XX (UNIL) UNILEVER NV.
PA (UNIL) UNILEVER PLC.
PA (HIND-) HINDUSTAN LEVER LTD.
PI Bodle EA, Van Der Velden S, De Vries CH, Wang H;
XX WPI: 2000-514528/46.
DR N-PSDB; AAA50018, AAA50019.
XX Detergent composition comprising novel phenol oxidizing enzyme obtained
PT from fungus or bacteria, useful for pulp and paper bleaching, bleaching
PT color of stains on fabric and for anti-dye redeposition
XX
PS Claim 2; Fig 5A-B; 45pp; English.
XX The present sequence is that of a phenol oxidizing enzyme of
CC Stachybotrys chartarum MUCI 38898. A claimed detergent composition
CC comprises a phenol oxidizing enzyme having at least 60% identity to
CC the present sequence, and preferably obtained from a bacterium,
CC yeast or non-Stachybotrys fungus, especially Bipolaris spicifera,
CC Curvularia pallescens or Amorospodium atrum (see AAV95538-40). The
CC phenol oxidizing enzyme is capable of modifying the colour
CC associated with dyes or coloured compounds, and can be used for
CC pulp and paper bleaching, for bleaching the colour of stains on
CC fabric and for anti-dye transfer in detergent and textile
CC applications. It may also be capable of modifying the colour in
CC the absence or presence of an enhancer. Expression vectors and
CC host cells comprising a nucleic acid encoding a phenol oxidizing
CC enzyme, methods for producing the phenol oxidizing enzyme, and
CC methods for constructing expression hosts are provided.
XX
SQ Sequence 594 AA;
Query Match 100.0%; Score 3189; DB 21; Length 594;
Best Local Similarity 100.0%; Pred. No. 2.9e-299;
Matches 594; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 1 MLEKSWQLAAASGLSGVIGIPMDTGSHPLEAVDPKKTIVFADSLIAAGDDWESPPY 60
QY 1 MLEKSWQLAAASGLSGVIGIPMDTGSHPLEAVDPKKTIVFADSLIAAGDDWESPPY 60
1 MLEKSWQLAAASGLSGVIGIPMDTGSHPLEAVDPKKTIVFADSLIAAGDDWESPPY 60
Db 61 NLLYRNALPIPPKOPKMITTNPVTGKDIYVEIETIKPQORITPTLRPATLVGYDGMSP 120
QY 61 NLLYRNALPIPPKOPKMITTNPVTGKDIYVEIETIKPQORITPTLRPATLVGYDGMSP 120
1 NLLYRNALPIPPKOPKMITTNPVTGKDIYVEIETIKPQORITPTLRPATLVGYDGMSP 120
Db 61 NLLYRNALPIPPKOPKMITTNPVTGKDIYVEIETIKPQORITPTLRPATLVGYDGMSP 120
QY 121 GPTFNVRGTETVVRFINNATVENSVLHSGSPSRAPFDGWAEDVTPEGEYKDYFFPYQS 180

Db 121 GPTFNVRGTETVVRFINNATVENSVLHSGSPSRAPFDGWAEDVTPEGEYKDYFFPYQS 180

QY 181 ARLIMYDHAFMKTAENAYFGAGAYIINDEADALGPGCYGFDIPLITAKYVADG 240
Db 181 ARLIMYDHAFMKTAENAYFGAGAYIINDEADALGPGCYGFDIPLITAKYVADG 240
QY 241 TLNSTEGEDDLMGDVHVNGQPPFLNVOPRKYRFRFLNAAVSRWLVLVPTSSPNVR 300
Db 241 TLNSTEGEDDLMGDVHVNGQPPFLNVOPRKYRFRFLNAAVSRWLVLVPTSSPNVR 300
QY 301 IPFGVIASDAGLLQAPVQTSNLVLAVEREIIIDFTNFAQOTLDLRNVAETNDVGEDE 360
Db 301 IPFGVIASDAGLLQAPVQTSNLVLAVEREIIIDFTNFAQOTLDLRNVAETNDVGEDE 360
QY 361 YARTLEVMRVYSSGTVEDNSQVSTLRDVPFPPKGPADKHKFRSNGHYLINDVG 420
Db 361 YARTLEVMRVYSSGTVEDNSQVSTLRDVPFPPKGPADKHKFRSNGHYLINDVG 420
QY 421 ADVNERVLAKPELGTEVWELENSGGMSHPVHILVDFTIKRTGGRGOVMPESAGLK 480
Db 421 ADVNERVLAKPELGTEVWELENSGGMSHPVHILVDFTIKRTGGRGOVMPESAGLK 480
QY 481 DVMWLGREGTLTIEAHYQPTGAYMWHCHNLIHEDNDMAVFNTYAMEEKGYLOEDFEDP 540
Db 481 DVMWLGREGTLTIEAHYQPTGAYMWHCHNLIHEDNDMAVFNTYAMEEKGYLOEDFEDP 540
QY 541 MNPKRAVPYNRNDFHARAGNFSAESITARVOELAEDEPYNRLEIDEDGIEE 594
Db 541 MNPKRAVPYNRNDFHARAGNFSAESITARVOELAEDEPYNRLEIDEDGIEE 594

RESULT 4
AAV96761 standard; Protein: 594 AA.
ID AAV96761
AC AAV96761
DT 09-OCT-2000 (first entry)
XX Stachybotrys chartarum phenol oxidizing enzyme.
DE
XX
KM Phenol oxidizing enzyme; colour; dye; modification; detergent; stain;
KM pulp; paper bleaching.
XX
OS Stachybotrys chartarum.
PN MO200037654-A2.
XX
PD 29-JUN-2000.
XX
PF 20-DEC-1999; 99WO-US31009.
PR 23-DEC-1998; 98US-0220871.
PR 23-JUN-1999; 99US-0338723.
XX
PA (GENV) GENENCOR INT INC.
PI Wang H, Bodle EA;
XX
DR WPI: 2000-452191/39.
DR N-PSDB; AAA51313, AAA51314.
XX
PT New phenol oxidizing enzyme for modifying colors associated with dyes
PT or colored compounds, is obtained from fungus and is encoded by a
PT nucleic acid comprising a specific nucleotide sequence
XX
PS Claim 1; Fig 5A-B; 45pp; English.
XX This is the sequence of Stachybotrys chartarum phenol oxidizing enzyme.
CC Phenol oxidizing enzymes encoded by nucleic acid sequences which
CC hybridize to the coding DNA are claimed, as long as the enzyme is capable
CC of modifying the colour associated with dyes or coloured compounds. The

CC enzymes are useful in detergent compositions and for modifying colors
 CC associated with dyes or colored compounds which occur in stains in a
 CC sample. The enzymes are also useful for pulp and paper bleaching,
 CC anti-dye transfer in detergent and other textile applications.

XX Sequence 594 AA;

Query Match 100.0%; Score 3189; DB 21; Length 594;
 Best Local Similarity 100.0%; Pred. No. 2.9e-299;
 Matches 594; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLEKSMQIAAASGLISGLVIGIPMDTGSHPRIEAVDEPVKTEVFADSLAAAGDDMESPPY 60
 DB 1 MLEKSMQIAAASGLISGLVIGIPMDTGSHPRIEAVDEPVKTEVFADSLAAAGDDMESPPY 60
 QY 61 NLLYRNALPIPPVKOPKMIITNPVTKDIIWYEIEIKPFOQRIYPTLRPATLVGDGMS 120
 DB 61 NLLYRNALPIPPVKOPKMIITNPVTKDIIWYEIEIKPFOQRIYPTLRPATLVGDGMS 120
 QY 121 GPTFNVPKGTETVVFINNATVENSVHLHGSFSRAPFDGMADVTFFPEYKDYPPNQ 180
 DB 121 GPTFNVPKGTETVVFINNATVENSVHLHGSFSRAPFDGMADVTFFPEYKDYPPNQ 180
 QY 121 GPTFNVPKGTETVVFINNATVENSVHLHGSFSRAPFDGMADVTFFPEYKDYPPNQ 180
 DB 121 GPTFNVPKGTETVVFINNATVENSVHLHGSFSRAPFDGMADVTFFPEYKDYPPNQ 180
 QY 181 ARLLMYHDAEFKTAENAYFGGAGAYIINDEADALGPSYGEEDIPILITAKYYNADG 240
 DB 181 ARLLMYHDAEFKTAENAYFGGAGAYIINDEADALGPSYGEEDIPILITAKYYNADG 240
 QY 241 TLRSTEGEDQDLMGVIVHNGOPWPEFLVOPPKYRFRFLNAVSAMLLYLVRTSSPNVR 300
 DB 241 TLRSTEGEDQDLMGVIVHNGOPWPEFLVOPPKYRFRFLNAVSAMLLYLVRTSSPNVR 300
 QY 301 IPFOVIASDAGLLQAPVOTSNLYLAVERYEIITFTNFAQTDLRNVAAETNDVGDEDE 360
 DB 301 IPFOVIASDAGLLQAPVOTSNLYLAVERYEIITFTNFAQTDLRNVAAETNDVGDEDE 360
 QY 361 YARLLEVMRFVYSSGTVEDNSOVSTLRDVPPEPKKEGPADKHFEKSNHLYLINDVGF 420
 DB 361 YARLLEVMRFVYSSGTVEDNSOVSTLRDVPPEPKKEGPADKHFEKSNHLYLINDVGF 420
 QY 421 ADVNERVLAKPELGTVEVWELENSSGSHPVHILVDFKILKRTGGQVAPYESSAGLK 480
 DB 421 ADVNERVLAKPELGTVEVWELENSSGSHPVHILVDFKILKRTGGQVAPYESSAGLK 480
 QY 481 DVVWLGREGTELTIEAHYOPWTGAYVMHCHNLIHEDNDMAAFVNTAMEKGYLQEDFEDP 540
 DB 481 DVVWLGREGTELTIEAHYOPWTGAYVMHCHNLIHEDNDMAAFVNTAMEKGYLQEDFEDP 540
 QY 541 MNPKRAVPYRNDFHARAGNFSASITARVOELAEOPRYNRDLDEILDGIEE 594
 DB 541 MNPKRAVPYRNDFHARAGNFSASITARVOELAEOPRYNRDLDEILDGIEE 594

RESULT 5
 AA018210 standard: Protein; 594 AA.
 AC AA018210;
 DT 13-SEP-2002 (first entry)
 DE S chartarum phenol oxidizing enzyme.
 KW Phenol oxidizing enzyme; fungus; redox reaction; detergent;
 KW paper industry; pulp industry; textile; food industry.
 OS Stachybotrys chartarum.
 XX US6399329-B1.
 XX 04-JUN-2002.
 XX 21-DEC-1999; 99US-0468578.

PR 12-DEC-1996; 98US-0220871.
 PR 23-JUN-1999; 99US-0338723.
 XX
 PA (GENEW) GENENCOR INT INC.
 XX
 PI Wang H, Bodie EA.
 XX
 DR WPI; 2002-498835/53.
 DR N-PSDB; AAL47582, AAL47584.

PT New polynucleotides encoding phenol oxidizing enzymes, useful for
 PT preventing the transfer of dyes in solution from one textile to another
 PT during detergent washing -

Example 5; Fig 4; 37pp; English.

CC The present invention provides the protein and coding sequences of phenol
 CC oxidizing enzymes from Stachybotrys chartarum, Bipolaris spicifera and
 CC Curvularia pallens. These enzymes are useful in the textiles, paper,
 CC pulp, detergent and food industries. In particular they are useful for
 CC preventing the transfer of dyes in solution from one textile to another
 CC during detergent washing (dye transfer inhibition). The present sequence
 CC is the S. chartarum phenol oxidizing enzyme.

XX Sequence 594 AA;

Query Match 100.0%; Score 3189; DB 23; Length 594;
 Best Local Similarity 100.0%; Pred. No. 2.9e-299;
 Matches 594; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLEKSMQIAAASGLISGLVIGIPMDTGSHPRIEAVDEPVKTEVFADSLAAAGDDMESPPY 60
 DB 1 MLEKSMQIAAASGLISGLVIGIPMDTGSHPRIEAVDEPVKTEVFADSLAAAGDDMESPPY 60
 QY 61 NLLYRNALPIPPVKOPKMIITNPVTKDIIWYEIEIKPFOQRIYPTLRPATLVGDGMS 120
 DB 61 NLLYRNALPIPPVKOPKMIITNPVTKDIIWYEIEIKPFOQRIYPTLRPATLVGDGMS 120
 QY 121 GPTFNVPKGTETVVFINNATVENSVHLHGSFSRAPFDGMADVTFFPEYKDYPPNQ 180
 DB 121 GPTFNVPKGTETVVFINNATVENSVHLHGSFSRAPFDGMADVTFFPEYKDYPPNQ 180
 QY 181 ARLLMYHDAEFKTAENAYFGGAGAYIINDEADALGPSYGEEDIPILITAKYYNADG 240
 DB 181 ARLLMYHDAEFKTAENAYFGGAGAYIINDEADALGPSYGEEDIPILITAKYYNADG 240
 QY 241 TLRSTEGEDQDLMGVIVHNGOPWPEFLVOPPKYRFRFLNAVSAMLLYLVRTSSPNVR 300
 DB 241 TLRSTEGEDQDLMGVIVHNGOPWPEFLVOPPKYRFRFLNAVSAMLLYLVRTSSPNVR 300
 QY 301 IPFOVIASDAGLLQAPVOTSNLYLAVERYEIITFTNFAQTDLRNVAAETNDVGDEDE 360
 DB 301 IPFOVIASDAGLLQAPVOTSNLYLAVERYEIITFTNFAQTDLRNVAAETNDVGDEDE 360
 QY 361 YARLLEVMRFVYSSGTVEDNSOVSTLRDVPPEPKKEGPADKHFEKSNHLYLINDVGF 420
 DB 361 YARLLEVMRFVYSSGTVEDNSOVSTLRDVPPEPKKEGPADKHFEKSNHLYLINDVGF 420
 QY 421 ADVNERVLAKPELGTVEVWELENSSGSHPVHILVDFKILKRTGGQVAPYESSAGLK 480
 DB 421 ADVNERVLAKPELGTVEVWELENSSGSHPVHILVDFKILKRTGGQVAPYESSAGLK 480
 QY 481 DVVWLGREGTELTIEAHYOPWTGAYVMHCHNLIHEDNDMAAFVNTAMEKGYLQEDFEDP 540
 DB 481 DVVWLGREGTELTIEAHYOPWTGAYVMHCHNLIHEDNDMAAFVNTAMEKGYLQEDFEDP 540
 QY 541 MNPKRAVPYRNDFHARAGNFSASITARVOELAEOPRYNRDLDEILDGIEE 594
 DB 541 MNPKRAVPYRNDFHARAGNFSASITARVOELAEOPRYNRDLDEILDGIEE 594

RESULT 6
 AAY95538

ID		AA95538 standard; Protein; 627 AA.	
xx			
AC		AA95538;	
xx			
D7		10-OCT-2000 (first entry)	
xx			
DE	Bipolaris splicifera phenol oxidising enzyme.		
KW	Phenol oxidising enzyme; detergent; bleaching.		
OS	Bipolaris splicifera.		
PN	M0200039306-AZ.		
XX			
PF	06-JUL-2000.		
XX			
R	20-DEC-1999; 99MO-EPI0287.		
XX			
DR	23-DEC-1998; 98US-0220871.		
N	23-JUN-1999; 99US-0338723.		
PA	(UNITL) UNILEVER NV.		
PA	(UNITL) UNILEVER PLC.		
XI	(HIND-) HINDUSTAN LEVER LTD.		
FI	Bodde EA, Van Der Velden S, De Vries CH, Wang H,		
PS	WIJ, 2000-514528/46.		
PT	N-PSDB; AAA50020.		
XX			
XX			
Claim 8; Fig 3; 45pp; English.			
CC	The present sequence is that of the Bipolaris splicifera		
CC	phenol oxidising enzyme. The invention relates to detergent		
CC	compositions comprising novel phenol oxidising enzymes that have at		
CC	least 60% identity with the phenol oxidising enzyme of Stachybotrys		
CC	charitum (see AA95537), and which are obtained from a bacterium,		
CC	yeast or non-Stachybotrys fungus, especially B. splicifera.		
CC	Cuvularia pallescens (see AA95539) and Amerosporium atrum (see		
CC	AA95540). The phenol oxidising enzyme is capable of modifying the		
CC	colour associated with dyes or coloured compounds, and can be used		
CC	for pulp and paper bleaching, for colouring compounds, and can be used		
CC	fabric and for anti-dye transfer in detergent and textile		
CC	applications. It may also be capable of modifying the colour in		
CC	the absence or presence of an enhancer. Expression vectors and		
CC	host cells comprising a nucleic acid encoding a phenol oxidising		
CC	enzyme, methods for producing the phenol oxidising enzyme, and		
CC	methods for constructing expression hosts are provided.		
SQ			
Sequence	627 AA;		
OY	Query Match	61.3%; Score 1954.5; DB 21; Length 627;	
	Best Local Similarity	61.1%; Pred.No. 1e-179;	
	Matches 367; Conservative 79; Mismatches 134; Indels 21; Gaps 8		
Db			
6	LFSKLAALS--IAKGIVGAL--SERPAKFVDNTPDCKA--LASIVEDDPADVNMKL	53	
OY			
54	-DMSPPYNLLRNALPFPVKKPMITTNVTGVGDIIYYEIEIKRFOORIPYLRLPATL	112	
Db			
59	KDMQSPEPLFRGPLRPPIPKAKENK-LTNEVTKNKELMYIELVIKFFQQOYPISLRPARL	117	
OY			
113	VGYDGSGBPFLPNVRGTETVFRELNATVENSVHLGSSSPRAPFDGAEDVPFGEXKD	172	
Db			
118	VGYGISGPFTIIVPRGTFAVVRFINOGDRESSITHLGSSSPRAPFDDGMADIMKGEKYD	177	
OY			
173	YTFPYNSARILWMHDNAFMKTAFNAVYGAGAVTIINEADEBALGLPGCYGFDTPLIFT	232	
	::::: ::::: :::::		

Dd		178	YYPPNNOAARFLMYHNNAAHVTAENNAHYEGQAGATYLTTPRAEDALGLPSGCTKYDIPVLS	237
Qy		233	AKYVNADGTLRSTGEODDLMGVDVIHVNGOPWPLNVQPRXYRFRRLNAAVSRAMLLYLV	292
Dd		238	SKTYNMADGLTKTSVGEDKSWGDILHVNGQPWFLLNVDEPKRYRLRFMAAVSRNFALYFV	297
Qy		293	KISSPNVRIPFOVIASDAQLLCAPOTSMLYLAVAREIITIDPTNFGOTLDRVAET	352
Dd		298	KONNTATRIPEFOVLASDAGILTHRPVOTSMYVAAAEREIYVEFPAPYAGOTLDRNPAKA	357
Qy		353	NDDVEDEVARLTLEVMRFVSSGTVEDNSGVNSTLDVPDPCHKGPADKKFKFERENGH	412
Dd		358	NGIGTDDDDANDDKAKRRHFVVSSQTVDANSVYPEQLSQILOPADKT-DIDHHFRHRNGE	416
Qy		413	YLINDYGADVNERVLAKEPDLGTVEWMELNSSGGMSHPRHIIHLDFEKLRTGGRQ--	470
Dd		417	WRINGISGFADVNERVLAKVRPGCVLMELNSSGGMSHPRHIVHLVDPFVARYGDBETRQ	476
Qy		471	VMPYESAGLKDVWLGRGETLTITEAHYOPTGAYMHCHNLIHEDNDMAVFENVTAEEK	530
Dd		477	VMPYEAGAGLDVWLGRHEFTVLEAHYAPDWGMGYMFHCNHLIHEDQDMAAFDVTKLNF	536
Qy		531	GYSIQ-DEDEDPMNKRAVPYNRNDFHARAQFNFSASTARTAOELAQEPNRDELLED	589
Dd		537	GYNETTFHDPEDPRMSARPTRAGDLTARSGLFSEESIRARVNELALEOPYSELAQYTAS	596
Qy		590 L 590		
Dd		597 L 597		
<hr/>				
RESULT 7				
AAY96762 ID	AAY96762 standard; Protein; 627 AA.			
XX AC	AAV96762:			
XX DT	09-OCT-2000 (first entry)			
XX DE	Bipolaris spiciifera phenol oxidizing enzyme.			
KM KW	Phenol oxidizing enzyme; colour; dye; modification; detergent; stain;			
XX XX	pulp; paper bleaching.			
OS OS	Bipolaris spiciifera.			
PX PN	MO200037654-A2.			
XZ PD	29-JUN-2000.			
XX PF	20-DEC-1999; 99WO-USJ1009.			
ER ER	23-DEC-1998; 98US-0220871.			
XX PA	23-JUN-1999; 99US-0338723.			
PI PI	(GENEV) GENENCOR INT INC.			
XX DR	Wang H, Bodie EA;			
XX PS	WPI; 2000-452191/39.			
CC CC	N-PADB; AAA51315.			
CC CC	New phenol oxidizing enzyme for modifying colors associated with dyes or colored compounds, is obtained from fungus and is encoded by a nucleic acid comprising a specific nucleotide sequence			
CC CC	Claim 8; Fig 3; 45pp; English.			
This sequence is the Bipolaris spiciifera phenol oxidizing enzyme. Phenol oxidizing enzymes encoded by nucleic acid sequences which hybridize to the Stachybotrys chartarum DNA (AAA51313) are claimed, as long as the enzyme is capable of modifying the colour associated with dyes or coloured compounds. The enzymes are useful in detergent				

CC compositions and for modifying colors associated with dyes or coloured
CC compounds which occur in stains in a sample. The enzymes are also useful
CC for pulp and paper bleaching, anti-dye transfer in detergent and other
CC textile applications.

XX Sequence 627 AA;

Query Match 61.3%; Score 1954.5; DB 21; Length 627;
Best Local Similarity 61.1%; Pred. No. 1e-179;
Matches 367; Conservative 79; Mismatches 134; Indels 21; Gaps 8;

```
QY 2 LFKSMQLAAAGSLGSGVIGIPMDGSHPIEAVDEPVTEVRADSLAAAGD----- 53
DB 6 LFSALQLVLS---IAKGIYVAL--SERPAKVDNTPDEKAA--LASTVEDDPADVNM 58
QY 54 -DMESPYNLLRYNALPIPVKOPKMITNPTGKDIWYIEIKRPFQOARIYPLRPATL 112
DB 59 KDMQSPERPLIFRQPLPIPAKEPNK-LTNVTKKEIWEYIEIVIKPFQOYPSLRPARL 117
DB 113 VGIDGMSGPTFPNPRGTEYVVRFINNAVTENSVHLGSPSRAPFDGMAEDVTPPEGYKD 172
DB 118 VGYGDISGPTIIVPRGTEAVVRFINOGDRESSIHLGSPSRAPFDGMAEDVTPPEGYKD 177
QY 173 YTFPNYOSARLLMWDHAFMKTAENAYFGAGATYINDPADDALGSPGYGKDYDIPVLVS 232
DB 178 YTFPNYOSARLLMWDHAFMKTAENAYFGAGATYINDPADDALGSPGYGKDYDIPVLVS 237
QY 233 AKYNNADGTLRSTEGEDDGLMDVYIHVNGQPMPFLNVPKRYRFRFLNAAVSRAVLTYLV 292
DB 238 SKYYNADGTLRSTEGEDKSVMGDIIHVNGQPMPFLNVPKRYRFRFLNAAVSRAVLTYLV 297
QY 293 RTSSPNVRIIPPOVLAASDAGLLQAPVQTSNLYLAVEREYIITDFTNAGQTLDIRNAET 352
DB 298 KQDNTATRLPPOVLAASDAGLLTHPVQTSNLYLAVEREYIITDFTNAGQTLDIRNAET 357
QY 353 NDVDEDEYARTLEVMRNVVSSGTEVDNSOVPSTLRDVPFPKRGPAKDKFKPERSNGH 412
DB 358 NGIGTDDYANTDKVMRNVVSSGTEVDNSOVPSTLRDVPFPKRGPAKDKFKPERSNGH 416
QY 413 YLINDVGFADYNEERLAKPELGTEVEWELNENSSGWSHPVHILHVEFKILRTGGRGO-- 470
DB 417 WRINGIGFADYNEERLAKPELGTEVEWELNENSSGWSHPVHILHVEFKILRTGGRGO-- 476
QY 471 VMPYESAGLKDVVNLGRGETLITIAHYOPWTGAYMMCHNLIHEDNDMAAVENTAMEEK 530
DB 477 VMPYESAGLKDVVNLGRGETLITIAHYOPWTGAYMMCHNLIHEDNDMAAVENTAMEEK 536
QY 531 GYLQ-EDFEDPMNPKRAVPIPNRNDFAHAGNFSSESTARVOELADEPYNRLDEILED 589
DB 537 GYNETTFDHPEDPRMSARPEPTAGDLTARSGIFSEESIRAVNELALEOPISLAQVYAS 596
QY 590 L 590
DB 597 L 597
```

RESULT 8
AAO18211
ID AAO18211 standard; Protein: 627 AA.

XX AC AAO18211;

XX DT 13-SEP-2002 (first entry)

XX DE B spicifera phenol oxidizing enzyme.

XX KW Phenol oxidizing enzyme; fungus; redox reaction; detergent;

XX KM Paper industry; pulp industry; textile; food industry.

XX OS Bipolaris spicifera.

XX PN US6399329-B1.

PD 04-JUN-2002.

XX 21-DEC-1999; 99US-0468578.

XX 12-DEC-1998; 98US-0220871.

XX 23-JUN-1999; 99US-0338723.

XX (GENEV) GENENCOR INT INC.

XX Wang H, Bodle EA;

XX WPI: 2002-496835/53.

XX N-PSDB: AAL47583.

XX New polynucleotides encoding phenol oxidizing enzymes, useful for

XX preventing the transfer of dyes in solution from one textile to another

XX during detergent washing -

XX Claim 1; Fig 3; 37pp; English.

CC The present invention provides the protein and coding sequences of phenol
CC oxidizing enzymes from Stachybotrys chartarum, Bipolaris spicifera and
CC Curvularia pallescens. These enzymes are useful in the textiles, paper,
CC pulp, detergent and food industries. In particular they are useful for
CC preventing the transfer of dyes in solution from one textile to another
CC during detergent washing (dye transfer inhibition). The present sequence
CC is the B. spicifera phenol oxidizing enzyme.

XX Sequence 627 AA;

Query Match 61.3%; Score 1954.5; DB 23; Length 627;
Best Local Similarity 61.1%; Pred. No. 1e-179;
Matches 367; Conservative 79; Mismatches 134; Indels 21; Gaps 8;

```
QY 2 LFKSMQLAAAGSLGSGVIGIPMDGSHPIEAVDEPVTEVRADSLAAAGD----- 53
DB 6 LFSALQLVLS---IAKGIYVAL--SERPAKVDNTPDEKAA--LASTVEDDPADVNM 58
QY 54 -DMESPYNLLRYNALPIPVKOPKMITNPTGKDIWYIEIKRPFQOARIYPLRPATL 112
DB 59 KDMQSPERPLIFRQPLPIPAKEPNK-LTNVTKKEIWEYIEIVIKPFQOYPSLRPARL 117
QY 113 VGIDGMSGPTFPNPRGTEYVVRFINNAVTENSVHLGSPSRAPFDGMAEDVTPPEGYKD 172
DB 118 VGYGDISGPTIIVPRGTEAVVRFINOGDRESSIHLGSPSRAPFDGMAEDVTPPEGYKD 177
QY 173 YTFPNYOSARLLMWDHAFMKTAENAYFGAGATYINDPADDALGSPGYGKDYDIPVLVS 232
DB 178 YTFPNYOSARLLMWDHAFMKTAENAYFGAGATYINDPADDALGSPGYGKDYDIPVLVS 237
QY 233 AKYNNADGTLRSTEGEDDGLMDVYIHVNGQPMPFLNVPKRYRFRFLNAAVSRAVLTYLV 292
DB 238 SKYYNADGTLRSTEGEDKSVMGDIIHVNGQPMPFLNVPKRYRFRFLNAAVSRAVLTYLV 297
QY 293 RTSSPNVRIIPPOVLAASDAGLLQAPVQTSNLYLAVEREYIITDFTNAGQTLDIRNAET 352
DB 298 KQDNTATRLPPOVLAASDAGLLTHPVQTSNLYLAVEREYIITDFTNAGQTLDIRNAET 357
QY 353 NDVDEDEYARTLEVMRNVVSSGTEVDNSOVPSTLRDVPFPKRGPAKDKFKPERSNGH 412
DB 358 NGIGTDDYANTDKVMRNVVSSGTEVDNSOVPSTLRDVPFPKRGPAKDKFKPERSNGH 416
QY 413 YLINDVGFADYNEERLAKPELGTEVEWELNENSSGWSHPVHILHVEFKILRTGGRGO-- 470
DB 417 WRINGIGFADYNEERLAKPELGTEVEWELNENSSGWSHPVHILHVEFKILRTGGRGO-- 476
QY 471 VMPYESAGLKDVVNLGRGETLITIAHYOPWTGAYMMCHNLIHEDNDMAAVENTAMEEK 530
DB 477 VMPYESAGLKDVVNLGRGETLITIAHYOPWTGAYMMCHNLIHEDNDMAAVENTAMEEK 536
QY 531 GYLQ-EDFEDPMNPKRAVPIPNRNDFAHAGNFSSESTARVOELADEPYNRLDEILED 589
DB 537 GYNETTFDHPEDPRMSARPEPTAGDLTARSGIFSEESIRAVNELALEOPISLAQVYAS 596
```


XX	Claim 8; Fig 10; 45pp; English.
PS	
vv	

This sequence is the Curvularia pallescens phenol oxidizing enzyme. Phenol oxidizing enzymes encoded by nucleic acid sequences which hybridize to the *Stachybotrys chartarum* DNA (AA51313) are claimed, as long as the enzyme is capable of modifying the colour associated with dyes or coloured compounds. The enzymes are useful in detergent compositions and for modifying colors associated with dyes or coloured compounds which occur in stains in a sample. The enzymes are also useful for pulp and paper bleaching, anti-dye transfer in detergent and other textile applications.

50 Sequence 627 AA;

Query Match	Score	DB	Length
60.58;	1929.5;	21;	627;
Best Local Similarity	60.58;	Docid No. 360-177.	

Best Local Similarity 60.5%; Pred. No. 2.6e-177;

Matches 364; Conservative 81; Mismatches 134; Indels 23; Gaps 9;

[illegible]

Search completed: July 1, 2003, 10:38:51
Job time : 75 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: July 1, 2003, 10:37:36 ; Search time 26 Seconds
(Without alignments)
672.201 Million cell updates/sec

Title: US-10-080-233-2

Perfect score: 3189
Sequence: 1 MLEFSWQLAASGLSGVLG.....AEQPYRDLDELIDGIEE 594

Scoring table:

BLOSUM62
Gapop 10.0 , Gapext 0.5

Number of hits satisfying chosen parameters: 262574

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database:

Issued Patents AA:
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2: /cgml2_6/p10data/1/aa/5B.COMB.pep.*
3: /cgml2_6/p10data/1/aa/6A.COMB.pep.*
4: /cgml2_6/p10data/1/aa/6B.COMB.pep.*
5: /cgml2_6/p10data/1/aa/PCITUS.COMB.pep.*
6: /cgml2_6/p10data/1/aa/backfile1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	3189	100.0	594	US-09-468-578-2	Sequence 2, Appl1
2	3189	100.0	594	US-09-468-578-2	Sequence 2, Appl1
3	1954.5	61.3	627	US-09-468-578-4	Sequence 4, Appl1
4	1929.5	54.1	627	US-09-468-578-7	Sequence 7, Appl1
5	1724.5	50.1	572	US-09-401-476-2	Sequence 4, Appl1
6	1716.5	53.8	583	US-09-401-476-2	Sequence 2, Appl1
7	1712.5	53.7	588	US-09-218-702-4	Sequence 4, Appl1
8	400.5	12.6	322	US-09-134-001C-2946	Sequence 2946, Ap
9	357.5	11.2	114	US-09-468-578-9	Sequence 9, Appl1
10	202	6.3	616	US-08-749-882A-2	Sequence 2, Appl1
11	202	6.3	616	US-08-539-134-2	Sequence 2, Appl1
12	202	6.3	616	US-08-991-531-2	Sequence 2, Appl1
13	202	6.3	616	US-09-032-315-9	Sequence 9, Appl1
14	202	6.3	616	US-08-993-318A-9	Sequence 9, Appl1
15	202	6.3	616	US-09-028-887-2	Sequence 2, Appl1
16	202	6.3	616	US-09-399-886-9	Sequence 9, Appl1
17	202	6.3	616	US-09-396-260-9	Sequence 9, Appl1
18	202	6.3	616	US-09-518-901-2	Sequence 2, Appl1
19	202	6.3	616	US-09-576-281-9	Sequence 9, Appl1
20	198.5	6.2	529	US-08-172-331B-14	Sequence 14, Appl1
21	198.5	6.2	529	US-08-706-037-25	Sequence 25, Appl1
22	198.5	6.2	529	US-09-005-397-25	Sequence 25, Appl1
23	198.5	6.2	529	US-09-032-315-5	Sequence 5, Appl1
24	198.5	6.2	529	US-08-993-318A-5	Sequence 5, Appl1
25	198.5	6.2	529	US-09-399-886-5	Sequence 5, Appl1
26	198.5	6.2	529	US-09-396-260-5	Sequence 5, Appl1
27	198.5	6.2	529	US-09-576-281-5	Sequence 5, Appl1

28	198	6.2	620	1	US-08-940-661A-2	Sequence 2, Appl1
29	198	6.2	620	2	US-09-083-485-2	Sequence 2, Appl1
30	198	6.2	620	2	US-08-939-218A-2	Sequence 2, Appl1
31	197	6.2	573	2	US-08-991-531-1	Sequence 1, Appl1
32	197	6.2	573	2	US-09-032-315-10	Sequence 10, Appl1
33	197	6.2	573	3	US-08-993-318A-10	Sequence 10, Appl1
34	197	6.2	573	3	US-09-028-887-1	Sequence 1, Appl1
35	197	6.2	573	4	US-09-399-886-10	Sequence 10, Appl1
36	197	6.2	573	4	US-09-396-260-10	Sequence 10, Appl1
37	197	6.2	573	4	US-09-518-901-1	Sequence 1, Appl1
38	197	6.2	573	4	US-09-576-281-10	Sequence 10, Appl1
39	197	6.2	616	5	PCT-US95-06816-2	Sequence 27, Appl1
40	197	6.2	620	1	US-08-706-037-27	Sequence 27, Appl1
41	197	6.2	620	2	US-09-005-397-27	Sequence 27, Appl1
42	197	6.2	620	5	PCT-US95-06815-2	Sequence 2, Appl1
43	194	6.1	511	1	US-08-462-484-8	Sequence 8, Appl1
44	194	6.1	511	1	US-08-441-147-8	Sequence 8, Appl1
45	194	6.1	511	5	PCT-US95-07536-8	Sequence 8, Appl1

ALIGNMENTS

RESULT 1	US-09-468-578-2	Sequence 2, Application US/09468578
Patent No. 6399329		
GENERAL INFORMATION:		
APPLICANT:	Wang, Huaming	
INVENTOR:	Bodde, Elizabeth A.	
TITLE OF INVENTION:	Phenol Oxidizing Enzymes	
FILE REFERENCE:	GC561-3	
CURRENT APPLICATION NUMBER:	US/09/468,578	
PRIOR FILING DATE:	1999-12-21	
PRIOR APPLICATION NUMBER:	US 09/220,871	
PRIOR FILING DATE:	1998-12-23	
PRIOR APPLICATION NUMBER:	US 09/338,723	
NUMBER OF SEQ ID NOS:	1999-06-23	
SOFTWARE:	FastSeq for Windows Version 4.0	
SEQ ID NO 2		
LENGTH:	594	
TYPE:	PRT	
ORGANISM:	Stachybotrys chartarum	
US-09-468-578-2		
Query Match	100.0%; Score 3189; DB 4; Length 594;	
Best Local Similarity	100.0%; Pred. No. 1.5e-308;	
Matches	594; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	
QY	1 MLEFSWQLAASGLSGVLGIPMDTGSHPITAVPEVKTETFAADSLAAGDDWESP	60
DB	1 MLEFSWQLAASGLSGVLGIPMDTGSHPITAVPEVKTETFAADSLAAGDDWESP	60
QY	61 NLTARNLPPIPVKQPMITINPTGDIWYEIEIRFOQRIPTLRPATLVGDS	120
DB	61 NLTARNLPPIPVKQPMITINPTGDIWYEIEIRFOQRIPTLRPATLVGDS	120
QY	121 GPTFNVRGTEITVVFRTNATVENSVLHSGSPAPDGAEDVTFPEKDYFPN	180
DB	121 GPTFNVRGTEITVVFRTNATVENSVLHSGSPAPDGAEDVTFPEKDYFPN	180
QY	181 ARLLMYDHPFMTKAENAFVGSQACAYIINDAEALGIPSGEFDIPLITATY	240
DB	181 ARLLMYDHPFMTKAENAFVGSQACAYIINDAEALGIPSGEFDIPLITATY	240
QY	241 TLRTEGEDDLMGDVIVHNGQPPFLNVQPRKRYRFLNAAVSRAMLVLR	300
DB	241 TLRTEGEDDLMGDVIVHNGQPPFLNVQPRKRYRFLNAAVSRAMLVLR	300
QY	301 IPRVYASDAGLLQAPVQTSNLYLAVEREIIITDFINAGQITDLRNAVET	360
DB	301 IPRVYASDAGLLQAPVQTSNLYLAVEREIIITDFINAGQITDLRNAVET	360

Query Match 100.0%; Score 3189; DB 4; Length 594;
Best Local Similarity 100.0%; Pred. No. 1.5e-308;
Matches 594; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Query 1 MLFQWOLAAAGSLGVLGIPMDGSHPIEAVDPEVTEVADSLAAAGDDMESPPY 60
1 MLFQWOLAAAGSLGVLGIPMDGSHPIEAVDPEVTEVADSLAAAGDDMESPPY 60
Db 1 MLFQWOLAAAGSLGVLGIPMDGSHPIEAVDPEVTEVADSLAAAGDDMESPPY 60

Query 61 NLTYNNALPIPPVKQPKMITNPVTGKDIWYEIEIKRFOQRITPRLRPATLVGDGMS 120
61 NLTYNNALPIPPVKQPKMITNPVTGKDIWYEIEIKRFOQRITPRLRPATLVGDGMS 120
Db 61 NLTYNNALPIPPVKQPKMITNPVTGKDIWYEIEIKRFOQRITPRLRPATLVGDGMS 120

Query 121 GPTFNVPRGTEVTVRFINNATVENSVLHGSPSRAPFDGMAEDVTFPGEEKDYFPPNQS 180
121 GPTFNVPRGTEVTVRFINNATVENSVLHGSPSRAPFDGMAEDVTFPGEEKDYFPPNQS 180
Db 121 GPTFNVPRGTEVTVRFINNATVENSVLHGSPSRAPFDGMAEDVTFPGEEKDYFPPNQS 180

Query 181 ARLLYHHAHAFKMTAKENAVFGQAGAYIINDEADALGIPSGYGEEDIPILITAKYNNMG 240
181 ARLLYHHAHAFKMTAKENAVFGQAGAYIINDEADALGIPSGYGEEDIPILITAKYNNMG 240
Db 181 ARLLYHHAHAFKMTAKENAVFGQAGAYIINDEADALGIPSGYGEEDIPILITAKYNNMG 240

Query 241 TLRTSGEGDODLMDGVIVHNGQPMPLVNOQPKYRFRFLNAVSRAMLLYLVTSSPNVR 300
241 TLRTSGEGDODLMDGVIVHNGQPMPLVNOQPKYRFRFLNAVSRAMLLYLVTSSPNVR 300
Db 241 TLRTSGEGDODLMDGVIVHNGQPMPLVNOQPKYRFRFLNAVSRAMLLYLVTSSPNVR 300

Query 301 IPFOVIASDAGILQAPVOTSNLYLAVEREYIITDFTNFAQTLDLRNVAETNDVDEDE 360
301 IPFOVIASDAGILQAPVOTSNLYLAVEREYIITDFTNFAQTLDLRNVAETNDVDEDE 360
Db 301 IPFOVIASDAGILQAPVOTSNLYLAVEREYIITDFTNFAQTLDLRNVAETNDVDEDE 360

Query 361 YARTLEVNRFFVSSSTVEDNSQVSTLNDVPPRPKKEGPAKHFFERSNGHYLLINDVGF 420
361 YARTLEVNRFFVSSSTVEDNSQVSTLNDVPPRPKKEGPAKHFFERSNGHYLLINDVGF 420
Db 361 YARTLEVNRFFVSSSTVEDNSQVSTLNDVPPRPKKEGPAKHFFERSNGHYLLINDVGF 420

Query 421 ADVNERVLAKPELGIVEVWELENSGSGMHPVHILVDPKILKRTGRCQVMPYESAGIK 480
421 ADVNERVLAKPELGIVEVWELENSGSGMHPVHILVDPKILKRTGRCQVMPYESAGIK 480
Db 421 ADVNERVLAKPELGIVEVWELENSGSGMHPVHILVDPKILKRTGRCQVMPYESAGIK 480

Query 481 DVVWLGREGETLITIEAHYQPMTGAYMMHCHNLIHEDNDMAAVFNVTAMEEKGYLOEDFEDP 540
481 DVVWLGREGETLITIEAHYQPMTGAYMMHCHNLIHEDNDMAAVFNVTAMEEKGYLOEDFEDP 540
Db 481 DVVWLGREGETLITIEAHYQPMTGAYMMHCHNLIHEDNDMAAVFNVTAMEEKGYLOEDFEDP 540

Query 541 MNPKRAVAYPNRNDPHARAGNFSASITARVOELAEORPYNRDLDELIDGIEE 594
541 MNPKRAVAYPNRNDPHARAGNFSASITARVOELAEORPYNRDLDELIDGIEE 594
Db 541 MNPKRAVAYPNRNDPHARAGNFSASITARVOELAEORPYNRDLDELIDGIEE 594

RESULT 2
Sequence 2, Application us/09218702
Patent No. 6426410
GENERAL INFORMATION:
APPLICANT: Mada, Huming
TITLE OF INVENTION: No. 6426410el Phenol Oxidizing Enzymes
FILE REFERENCE: GC567
CURRENT APPLICATION NUMBER: US/09/218,702
PRIORITY FILING DATE: 1998-12-22
NUMBER OF SEQ ID NOS: 5
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 2
LENGTH: 594
TYPE: PRT
ORGANISM: Stachybotrys sp.
US-09-218-702-2

Query Match 61.3%; Score 1954.5; DB 4; Length 627;
Best Local Similarity 61.1%; Pred. No. 1.3e-185;
Matches 367; Conservative 79; Mismatches 134; Indels 21; Gaps 8;

Query 2 LFKSQOLAAAGSLGVLGIPMDGSHPIEAVDPEVTEVADSLAAAGDDMESPPY 53
2 LFKSQOLAAAGSLGVLGIPMDGSHPIEAVDPEVTEVADSLAAAGDDMESPPY 53
Db 2 LFKSQOLAAAGSLGVLGIPMDGSHPIEAVDPEVTEVADSLAAAGDDMESPPY 53

Query 54 -DMESPNNLYRNALPIPPVKQPKMITNPVTGKDIWYEIEIKRFOQRITPRLRPATLV 112
54 -DMESPNNLYRNALPIPPVKQPKMITNPVTGKDIWYEIEIKRFOQRITPRLRPATLV 112
Db 54 -DMESPNNLYRNALPIPPVKQPKMITNPVTGKDIWYEIEIKRFOQRITPRLRPATLV 112

Query 113 VGYDMSGPTFNVPRGTEVTVRFINNATVENSVLHGSPSRAPFDGMAEDVTFPGEEKD 172
113 VGYDMSGPTFNVPRGTEVTVRFINNATVENSVLHGSPSRAPFDGMAEDVTFPGEEKD 172
Db 113 VGYDMSGPTFNVPRGTEVTVRFINNATVENSVLHGSPSRAPFDGMAEDVTFPGEEKD 172

Query 173 YTFPNYQASRLIWDHAFKMTAKENAVFGQAGAYIINDEADALGIPSGYGEEDIPILIT 232
173 YTFPNYQASRLIWDHAFKMTAKENAVFGQAGAYIINDEADALGIPSGYGEEDIPILIT 232
Db 173 YTFPNYQASRLIWDHAFKMTAKENAVFGQAGAYIINDEADALGIPSGYGEEDIPILIT 232

Query 233 AKYNAADGTLRTSGEGDODLMDGVIVHNGQPMPLVNOQPKYRFRFLNAVSRAMLLYL 292
233 AKYNAADGTLRTSGEGDODLMDGVIVHNGQPMPLVNOQPKYRFRFLNAVSRAMLLYL 292
Db 233 AKYNAADGTLRTSGEGDODLMDGVIVHNGQPMPLVNOQPKYRFRFLNAVSRAMLLYL 292

Query 293 RTSSPNVRIIPFOVIASDAGILQAPVOTSNLYLAVEREYIITDFTNFAQTLDLRNVAET 352
293 RTSSPNVRIIPFOVIASDAGILQAPVOTSNLYLAVEREYIITDFTNFAQTLDLRNVAET 352
Db 293 RTSSPNVRIIPFOVIASDAGILQAPVOTSNLYLAVEREYIITDFTNFAQTLDLRNVAET 352

Query 353 NDVGEDEYARTLEVNRFFVSSSTVEDNSQVSTLNDVPPRPKKEGPAKHFFERSNGHYLL 412
353 NDVGEDEYARTLEVNRFFVSSSTVEDNSQVSTLNDVPPRPKKEGPAKHFFERSNGHYLL 412
Db 353 NDVGEDEYARTLEVNRFFVSSSTVEDNSQVSTLNDVPPRPKKEGPAKHFFERSNGHYLL 412

Query 413 YLINDVGRADVNERVLAKPELGIVEVWELENSGSGMHPVHILVDPKILKRTGRCQV 470
413 YLINDVGRADVNERVLAKPELGIVEVWELENSGSGMHPVHILVDPKILKRTGRCQV 470
Db 413 YLINDVGRADVNERVLAKPELGIVEVWELENSGSGMHPVHILVDPKILKRTGRCQV 470

Query 471 VMPYESAGILKDVVWLGREGETLITIEAHYQPMTGAYMMHCHNLIHEDNDMAAVFNVTAMEEK 530
471 VMPYESAGILKDVVWLGREGETLITIEAHYQPMTGAYMMHCHNLIHEDNDMAAVFNVTAMEEK 530
Db 471 VMPYESAGILKDVVWLGREGETLITIEAHYQPMTGAYMMHCHNLIHEDNDMAAVFNVTAMEEK 530

Query 531 GYLO-EDFEDPNNPKRAVAYPNRNDPHARAGNFSASITARVOELAEORPYNRDLDELID 589
531 GYLO-EDFEDPNNPKRAVAYPNRNDPHARAGNFSASITARVOELAEORPYNRDLDELID 589
Db 531 GYLO-EDFEDPNNPKRAVAYPNRNDPHARAGNFSASITARVOELAEORPYNRDLDELID 589

Db 537 GYNETDFHDPEDPMSARPTAGDILARSIFSEESIRARVNELAEQPSYSLAQYAS 596
OY 590 L 590
Db 597 L 597

RESULT 4

US-09-468-578-7
; Sequence 7, Application US/09468578
; Patent No. 6393329
; GENERAL INFORMATION:
; APPLICANT: Wang, Huaming
; TITLE OF INVENTION: Phenol Oxidizing Enzymes
; FILE REFERENCE: GC561-3
; CURRENT APPLICATION NUMBER: US/09/468,578
; CURRENT FILING DATE: 1999-12-21
; PRIOR APPLICATION NUMBER: US 09/220,871
; PRIOR FILING DATE: 1998-12-23
; PRIOR APPLICATION NUMBER: US 09/338,723
; PRIOR FILING DATE: 1999-06-23
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 7
; LENGTH: 627
; TYPE: PRF
; ORGANISM: Curvularia pallescens.
US-09-468-578-7

Query Match 60.5%; Score 1929.5; DB 4; Length 627;
Best Local Similarity 60.5%; Pred. No. 3,9e-183;
Matches 364; Conservative 81; Mismatches 134; Indels 23; Gaps 9;

OY 2 LFSKOLAASGLSGVLGIPMDTGHPIEAVDPEKTEVFADSLAAGD----- 53
Db 6 LFSALDAS---IAKGIYVAL--SERPAKYIDETDEEKAA--LAAIVDDPADVPRIL 58
OY 54 -DSEPPYNNLYRNALPIPVKOPKMITNPVTGKDIWYIEIKPFOQRIYPTLRPATL 112
Db 59 KDMOSPBYPLFREALPIPAKEPK-MNPVTNKEIWEIYIKPNQOYTSLRARL 117
OY 113 VGYDGSPPGFENVPRGTETVRFINNATVENSVHLGSPSRAPFDGMAEDVTPGEGYKD 172
Db 118 VGDGISPPGTIYPRGTEAVRFVNOGDRESSIHLGSPSRAPFDGMAEDLWKQGFKD 177
OY 173 YFPPNQSARLLWYHHAFAFKTAENAFYGAAGAYIINDEADALGSPSGEPIPLIT 232
Db 178 YFPPNQAARFLWYHHAFAFKTAENAFYGAAGAYIITDPAEDALGSPSGYKDYDIPYLS 237
OY 233 AKYNNADGTLRSTEGEDODLMDGVIHVNGOPMPFLANVOPRRYPRFLNAVSRAMLTYLV 292
Db 238 SKRYNSDGTQTSVGEDNSLMDGVIHVNGOPMPFENVPRKRLRFLNAAVSRNFALYFV 297
OY 293 RISSPVNRIPEFOYIASDAGLLQAPVOTSNLYLAVERXEIITIDTFNAGOTLDRVAET 352
Db 298 KQATATRLPEFOYIASDAGLLTHPVQTSIDYVAAEXEYIYDFAPYAGOTIDLRNPAKA 357
OY 353 NDVGDEDEYARTLEVAFVYSSGTVEDNSQVPSLRLVPRPPRKEGADKHFKERSNGH 412
Db 358 NGVGTDDDYANTKRFHVSQAVVYDINSVPAQLSQIOPPAKTG-IDHHRFRHRTNSE 416
OY 413 YLLNDVGFADVNERVLAKPELGTVIEWELENSSGSGMHPVHILHYDKIILKRGSG--RG 469
Db 417 WRINGIGFADVQRIILAKVPRGTVEIWELENSSGSGMHPVHILHYDVRVYAKTGDESTRG 476
OY 470 QVAPYESAGLKDVYVLMGEGTLTTEAHYOPWTGAYMMHCNLIHEDNDMAVFNVTAMEE 529
Db 477 -VAPYESAGLKDVYVLMGEGTLTTEAHYOPWTGAYMMHCNLIHEDNDMAVFNVTAMEE 535
OY 530 KGYLQ-EDFEDPMNPKRAVPYKRNDFHARAGNFSASITARVOELAEQPSYSLAQYAS 588
Db 536 FGNETTDFHDPEDPMSARPTAGDILARSIFSEESIRARVNELAEQPSYSLAQYAS 595

OY 589 DL 590
Db 596 SL 597

RESULT 5

US-09-401-476-4
; Sequence 4, Application US/09401476
; Patent No. 6168936
; GENERAL INFORMATION:
; APPLICANT: Wang, Huaming
; TITLE OF INVENTION: No. 6168936el Phenol Oxidizing Enzymes
; FILE REFERENCE: GC584
; CURRENT APPLICATION NUMBER: US/09/401,476
; CURRENT FILING DATE: 1999-09-22
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 4
; LENGTH: 572
; TYPE: PRF
; ORGANISM: Stachyotrys charatum
US-09-401-476-4

Query Match 54.1%; Score 1724.5; DB 4; Length 572;
Best Local Similarity 60.3%; Pred. No. 8.6e-163;
Matches 322; Conservative 75; Mismatches 128; Indels 9; Gaps 7;

OY 57 SPPYNNLYRNALPIPVKOPKMITNPVTGKDIWYIEIKPFOQRIYPTLRPATLVGYD 116
Db 43 SPQYP-MFTVPLPIPVKOPRLVTNPNVNGOEIWEIYEFYHQYVPDLGSDLVGYD 101
OY 117 GMSPPGFENVPRGTETVRFINNATVENSVHLGSPSRAPFDGMAEDVTPGEGYKYYP 176
Db 102 GMSPPGFENVPRGTETVRFINNATVENSVHLGSPSRAPFDGMAEDVTPGEGYKYYP 161
OY 177 NYQSARLLWYHHAFAFKTAENAFYGAAGAYIINDEADALGSPSGEPIPLITLAKY 236
Db 162 NROGARLWYHHAFAFKTAENAFYGAAGAYIINDEADALGSPSGEPIPLITLAKY 221
OY 237 NADGTLRSTEGEDODLMDGVIHVNGOPMPFLANVOPRRYPRFLNAVSRAMLTYLVTS 296
Db 222 TANGLNLTYNGLNLSFNGDVIHVNGOPMPFENVPRKRLRFLNAAVSRNFALYFV 281
OY 297 PNVIPEOYVYASDAGLLQAPVOTSNLYLAVERXEIITIDTFNAGOTLDRVAET 355
Db 282 IDTLRPRKVLASDSGLLEHPRADTSLIISNAERIEVYFDSYAGKTIELRNLGSGIGI 341
OY 356 GDEDEYARTLEVAFVYSSGTVEDNSQVPSLRLVPRPPRKEGADKHFKERSNGHY 413
Db 342 GTDIDYDNTDKVMRFVVAADTTPDTSVVPANLMDVFPSPPTNTF--RQPRFGRTGPT 399
OY 414 LINDVGFADVNERVLAKPELGTVIEWELENSSGSGMHPVHILHYDKIILKRGSG--OY 471
Db 400 TINGVAFADVQNRILANVPVGTVERMELINAGNMTWHIHLVDFYISTSGNNARTV 459
OY 472 MPYSAGLKDVYVLMGEGTLTTEAHYOPWTGAYMMHCNLIHEDNDMAVFNVTAMEEK 531
Db 460 MPYES-GLKDVYVLMGEGTLTTEAHYOPWTGAYMMHCNLIHEDNDMAVFNVTAMEEK 518
OY 532 YLQDFEDPMNPKRAVPYKRNDFHARAGNFSASITARVOELAEQPSYSLAQYAS 585
Db 519 YNAVVFDPHMEIQLQARPELGTVIEWELENSSGSGMHPVHILHYDKIILKRGSG-- 572

RESULT 6

US-09-401-476-2
; Sequence 2, Application US/09401476
; Patent No. 6168936
; GENERAL INFORMATION:
; APPLICANT: Wang, Huaming
; TITLE OF INVENTION: No. 6168936el Phenol Oxidizing Enzymes
; FILE REFERENCE: GC584

Db 64 IODKTE-VSKLNTSKTKEDGTQGDVLVNGIVNRLTAKEERIKRLRLNGSNARDLNT 122
QY 290 YLVRTSSPNVRIPFOYIASDAGLLQAPVQTSNLYLVAERETIIDPTNAGOTLDLRNV 349
Db 123 KLSNNOS-----FETIASDQGLKNKAKLKEINLAPSEKEIVIDLSKKKGEKISL--- 173
QY 350 AETNDVDEDEYARTLEVMRFVSSGVTEEDNSQVPTLRDPPPHKEGPADEHFKERS 409
Db 174 -----VDNKK-----TVILPISNKEKSSNKGNTPK-----VSKRIKLEGM 208
QY 410 NGHYLINDVGFADYNERVLAKPELGTVEWELEN---SSGWSHPVHILVDKRIKRTG 466
Db 209 NDHVTINGNKF-DPN-RIDFTQKLNQKEWEIENVDKMGKMKHPEHIHGTQFKVLSDV 265
QY 467 GRCQVMPYESAGKDVWVGREGTFLTEAHYQPTGAYMMHCHNLHEDDMAVFTV 525
Db 266 --GEKPKDMRGKAKDVISLEPGQKALEVEFKN-TGYMHCHILHEHEDGMGQIKVT 321

ULT 9
09-468-578-9
Sequence 9, Application US/09468578
Patent No. 639329

GENERAL INFORMATION:
APPLICANT: Wang, Huang
APPLICANT: Bodie, Elizabeth A.
TITLE OF INVENTION: Phenol Oxidizing Enzymes
FILE REFERENCE: GC561-3
CURRENT APPLICATION NUMBER: US/09/468, 578
CURRENT FILING DATE: 1999-12-21
PRIOR APPLICATION NUMBER: US 09/220, 871
PRIOR FILING DATE: 1998-12-23
PRIOR APPLICATION NUMBER: US 09/338, 723
PRIOR FILING DATE: 1999-06-23
NUMBER OF SEQ ID NOS: 17
SOFTWARE: FASTSEQ for Windows Version 4.0
SEQ ID NO 9
LENGTH: 114
TYPE: PRF
ORGANISM: Amersporium atrum
NAME/KEY: VARIANT
LOCATION: (1)...(114)
OTHER INFORMATION: Xaa = space of unknown number of aa
US-09-468-578-9

Query Match 11.2%; Score 357.5; DB 4; Length 114;
Best Local Similarity 32.2%; Pred. No. 6.8e-28;
Matches 85; Conservative 13; Mismatches 15; Indels 151; Gaps 4;

Db 194 TBNATFGGAGAYIINDEADALGPSYGEFPIPLITPAKYNNADGTLSTEGEQDLM 253
1 TBNATFGGAGAYIINDEADALGPSYGEFPIPLITPAKYNNADGTLSTEGEQDLM 58
QY 254 GDVIVHNGQWPELNVQPKRYRFLNAAVSRAMLLYLVRTSSPNVRIPFOYIASDAGL 313
Db 59 GDVIVHNGQWPELNVQPKRYRFLNAAVSRAMLLYLVRTSSPNVRIPFOYIASDAGL 91
QY 314 QAPVQTSNLYLVAERETIIDPTNAGOTLDLRNVAETNDVDEDEYARTLEVMRFVS 373
Db 92 ----- 91
QY 374 SGTVEDNSQVPTLRDPPPHKEGPADEHFKERSNGHYLINDVGFADYNERVLAKPEL 433
Db 92 -----FK----- 93
QY 434 GTVEWELEN-SSGWSHPVHIL 456
Db 94 ---XVMELEWTSNGWSYVPHIL 114

RESULT 10
US-08-749-882A-2

Sequence 2, Application US/08749882A
Patent No. 5750388
GENERAL INFORMATION:
APPLICANT: Betka, Randy
APPLICANT: Thompson, Sheryl
APPLICANT: Xu, Feng
TITLE OF INVENTION: Purified Scytalidium Laccases
TITLE OF INVENTION: And Nucleic Acids Encoding Same
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
ADDRESS: No. 5750388Bk Of No. 5750388th America, Inc.
STREET: 405 Lexington Avenue - 64th Fl.
CITY: New York
STATE: NY
COUNTRY: USA
ZIP: 10174
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASTSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/749, 882A
FILING DATE: 15-NOV-1996
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Lambiris, Elias J
REGISTRATION NUMBER: 33,728
REFERENCE/DOCKET NUMBER: 4186, 020-US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-878-9652
TELEFAX: 212-878-9655
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 616 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
ORIGINAL SOURCE: Scytalidium thermophilum
US-08-749-882A-2

Query Match 6.3%; Score 202; DB 1; Length 616;
Best Local Similarity 23.1%; Pred. No. 3.4e-11;
Matches 147; Conservative 77; Mismatches 237; Indels 174; Gaps 35;

QY 8 LAAASGLL-SGVIGIPMDTGSHPLEAVDPVKEVFADSLAAAGDDWESPYNLYRN 66
Db 9 LLLAGLNSGALAAP---STHP--RSNPDLLEBDHSLTSRQG--SCHSPNRACWCS 61
QY 67 ALPIPPKQKMTITNPVTKDIIWYIEIKPQOQRIY--TLRPATLVIGDMSQPTF 124
Db 62 GFDINDYETK---TPNTGV-VRRYTFDTEVDNRGPGVVKEXMLINDKIL-GPTV 115
QY 125 NVDRGTETVYRFINN--ATVENSYHLHGSRRAP--FDGAEDVTF-----PGEYKDYFP 176
Db 116 FANWG-DTIEVYNNHILKRTGSIHMGHLQKGNINHDG-ANGTECPPIPGSSRYYSFR 173
QY 177 NYQSAIRLWYHDAFMKTAENAFYGGAGAYIINDEADALGPSYGEFPIPL-TLTK- 234
Db 174 ARQYG-TSMYHSH-FSAQYGN---GVSGALQINGPA---SLP-----YDIDGVLPLD 219
QY 235 --YNNADGTLRTEGEQDLMGVIAHNGO-----FWPLNVP--RKYRFRFLNAA 282
Db 220 WYKRSADQVLETLAKNAPFSDNYLINTAKHPTTGEGETAYVKLPDRHRRLINMS 279
QY 283 VSRAMLLYLVRTSSPNVRIPFOYIASDAGLLQAPVQTSNLYLVAERETIIDPT----- 337
Db 280 VENHFOVSLAKHT-----MYIADNVYNA-MYVDSLFMAVGQRYDITIDASAQVGN 331
QY 338 ---NFAQ-----TLDLRNAETN 353

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Db      332 YWENTTEGGQKCGFSHNPAPNAIFRYEGAPDALPTDGAAPKDHOCLDTIDLSPVYOKN 391
QY      354 DVGDEDEYARLTLEVARFVSSGTVEDNSQVPSTLRDVPFPKKEGPAKHFKEKERSNG-- 411
Db      392 -----VPVDFYKEPG-----NTLPVTL-----HVDQAAPHVFTWKINGS 428
QY      412 -----HYLINDVGFADVNERVLAKPELGTVWELENSSG--NSHPVHILV 457
Db      429 ADVDMDRPVLEEVYMNNDLSIPVKNNIIVRVDGVNEMTYWLVENDEGRSLPMPHLGH 488
QY      458 DEKILKRTGGRGQVMPYESAGL-----KDYVWL-GKGETLTIEAHYQ 498
Db      489 DFEVLGRS--PDVSPDSETRFVEDPAVDLPRLRGHNPVYKRDVTMLPARGWLLLAFTDN 545
QY      499 PWTGAYMMHCHNLIHEDNDMAVFNVTAMEEKGYL 533
Db      546 P--GAWLFRCHTAMHVSGLSVDFLERPDELRGOL 578

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GenCore version 5.1.6
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OM protein - protein search, using sw model

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(without alignments)
1277.063 Million cell updates/sec

Title: US-10-080-233-2

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424699 seqs, 109646833 residues

Total number of hits satisfying chosen parameters: 424699

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Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications-AA*

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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	3189	100.0	594	10	US-09-338-723A-2
2	3189	100.0	594	12	US-10-080-210-2
3	3189	100.0	594	12	US-10-080-233-2
4	1954.5	61.3	627	10	US-09-338-723A-4
5	1954.5	61.3	627	12	US-10-080-210-4
6	1724.5	54.1	572	9	US-09-942-185-4
7	1724.5	54.1	572	12	US-10-080-210-7
8	1716.5	53.8	583	9	US-09-942-185-2
9	1716.5	53.8	583	9	US-09-954-385-1
10	1712.5	53.7	568	12	US-10-080-233-4
11	500	15.7	511	9	US-09-738-626-4553
12	357.5	11.2	114	12	US-10-080-210-9
13	202	6.3	616	9	US-09-869-877-9
14	202	6.3	616	10	US-09-732-350-9
15	198.5	6.2	529	9	US-09-869-877-5
16	198.5	6.2	529	10	US-09-732-350-5
17	197	6.2	573	9	US-09-869-877-10
18	197	6.2	573	10	US-09-732-350-10
19	192.5	6.0	499	9	US-09-869-877-2

20	192.5	6.0	499	10	US-09-732-350-2	Sequence 2, Appl1
21	188.5	5.9	520	9	US-10-263-819-2	Sequence 2, Appl1
22	187.5	5.9	539	9	US-09-869-877-1	Sequence 1, Appl1
23	187.5	5.9	539	10	US-09-732-350-1	Sequence 1, Appl1
24	179	5.6	548	10	US-09-869-877-4	Sequence 4, Appl1
25	179	5.6	548	10	US-09-732-350-4	Sequence 4, Appl1
26	174.5	5.5	499	9	US-09-869-877-3	Sequence 3, Appl1
27	174.5	5.5	499	10	US-09-732-350-3	Sequence 3, Appl1
28	171.5	5.4	499	9	US-10-164-775-5	Sequence 5, Appl1
29	162	5.1	564	9	US-09-944-160-12	Sequence 12, Appl1
30	147	4.6	493	9	US-09-738-626-6780	Sequence 6780, Ap
31	126.5	4.0	572	10	US-09-869-877-7	Sequence 7, Appl1
32	126.5	4.0	572	10	US-09-732-350-7	Sequence 7, Appl1
33	121.5	3.8	886	9	US-10-002-3098-2	Sequence 2, Appl1
34	119.5	3.7	575	9	US-09-869-877-8	Sequence 8, Appl1
35	119.5	3.7	575	10	US-09-732-350-8	Sequence 8, Appl1
36	111	3.5	599	9	US-09-869-877-6	Sequence 6, Appl1
37	111	3.5	599	10	US-09-732-350-6	Sequence 6, Appl1
38	105	3.3	2764	9	US-09-808-602-80	Sequence 80, Appl1
39	105	3.3	2764	9	US-09-800-198-68	Sequence 68, Appl1
40	104.5	3.3	1938	9	US-10-014-436-2	Sequence 2, Appl1
41	103.5	3.2	596	9	US-10-213-990-51	Sequence 51, Appl1
42	103	3.2	19	10	US-09-338-723A-6	Sequence 6, Appl1
43	103	3.2	19	12	US-10-080-210-10	Sequence 10, Appl1
44	100.5	3.2	1600	9	US-09-738-626-4310	Sequence 4310, Ap
45	100.5	3.2	1653	10	US-09-741-669-402	Sequence 402, App

ALIGNMENTS

RESULT 1	US-09-338-723A-2	Sequence 2, Application US/09338723A
1	Patent No. US2002019038A1	GENERAL INFORMATION:
2	APPLICANT: Humming, Wang	TITLE OF INVENTION: Phenol Oxidizing Enzymes
3	FILE REFERENCE: GC561-2	CURRENT APPLICATION NUMBER: US/09/338,723A
4	CURRENT FILING DATE: 1999-06-23	PRIOR APPLICATION NUMBER: 09/220,871
5	PRIOR FILING DATE: 1998-12-23	NUMBER OF SEQ ID NOS: 11
6	SOFTWARE: FastSeq for Windows Version 3.0	SEQ ID NO 2
7	LENGTH: 594	TYPE: PRT
8	ORGANISM: Stachybotrys chartarum	Query Match
9	US-09-338-723A-2	Best local Similarity 100.0%; Score 3189; DB 10; Length 594;
10		Matches 594; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
11	1 MLFESWQLAASGLSGVLGIPMDTGSHPLEAVDPEVKTFFADSLAAGDDWESPYP 60	Sequence 2, Appl1
12	1 MLFESWQLAASGLSGVLGIPMDTGSHPLEAVDPEVKTFFADSLAAGDDWESPYP 60	Sequence 2, Appl1
13	1 MLFESWQLAASGLSGVLGIPMDTGSHPLEAVDPEVKTFFADSLAAGDDWESPYP 60	Sequence 1, Appl1
14	1 MLFESWQLAASGLSGVLGIPMDTGSHPLEAVDPEVKTFFADSLAAGDDWESPYP 60	Sequence 4, Appl1
15	1 MLFESWQLAASGLSGVLGIPMDTGSHPLEAVDPEVKTFFADSLAAGDDWESPYP 60	Sequence 4, Appl1
16	1 MLFESWQLAASGLSGVLGIPMDTGSHPLEAVDPEVKTFFADSLAAGDDWESPYP 60	Sequence 3, Appl1
17	1 MLFESWQLAASGLSGVLGIPMDTGSHPLEAVDPEVKTFFADSLAAGDDWESPYP 60	Sequence 5, Appl1
18	1 MLFESWQLAASGLSGVLGIPMDTGSHPLEAVDPEVKTFFADSLAAGDDWESPYP 60	Sequence 10, Appl1
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20	1 MLFESWQLAASGLSGVLGIPMDTGSHPLEAVDPEVKTFFADSLAAGDDWESPYP 60	Sequence 2, Appl1
21	1 MLFESWQLAASGLSGVLGIPMDTGSHPLEAVDPEVKTFFADSLAAGDDWESPYP 60	Sequence 2, Appl1
22	1 MLFESWQLAASGLSGVLGIPMDTGSHPLEAVDPEVKTFFADSLAAGDDWESPYP 60	Sequence 2, Appl1
23	1 MLFESWQLAASGLSGVLGIPMDTGSHPLEAVDPEVKTFFADSLAAGDDWESPYP 60	Sequence 2, Appl1
24	1 MLFESWQLAASGLSGVLGIPMDTGSHPLEAVDPEVKTFFADSLAAGDDWESPYP 60	Sequence 2, Appl1
25	1 MLFESWQLAASGLSGVLGIPMDTGSHPLEAVDPEVKTFFADSLAAGDDWESPYP 60	Sequence 2, Appl1
26	1 MLFESWQLAASGLSGVLGIPMDTGSHPLEAVDPEVKTFFADSLAAGDDWESPYP 60	Sequence 2, Appl1
27	1 MLFESWQLAASGLSGVLGIPMDTGSHPLEAVDPEVKTFFADSLAAGDDWESPYP 60	Sequence 2, Appl1
28	1 MLFESWQLAASGLSGVLGIPMDTGSHPLEAVDPEVKTFFADSLAAGDDWESPYP 60	Sequence 2, Appl1
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30	1 MLFESWQLAASGLSGVLGIPMDTGSHPLEAVDPEVKTFFADSLAAGDDWESPYP 60	Sequence 2, Appl1
31	1 MLFESWQLAASGLSGVLGIPMDTGSHPLEAVDPEVKTFFADSLAAGDDWESPYP 60	Sequence 2, Appl1
32	1 MLFESWQLAASGLSGVLGIPMDTGSHPLEAVDPEVKTFFADSLAAGDDWESPYP 60	Sequence 2, Appl1
33	1 MLFESWQLAASGLSGVLGIPMDTGSHPLEAVDPEVKTFFADSLAAGDDWESPYP 60	Sequence 2, Appl1
34	1 MLFESWQLAASGLSGVLGIPMDTGSHPLEAVDPEVKTFFADSLAAGDDWESPYP 60	Sequence 2, Appl1
35	1 MLFESWQLAASGLSGVLGIPMDTGSHPLEAVDPEVKTFFADSLAAGDDWESPYP 60	Sequence 2, Appl1
36	1 MLFESWQLAASGLSGVLGIPMDTGSHPLEAVDPEVKTFFADSLAAGDDWESPYP 60	Sequence 2, Appl1
37	1 MLFESWQLAASGLSGVLGIPMDTGSHPLEAVDPEVKTFFADSLAAGDDWESPYP 60	Sequence 2, Appl1
38	1 MLFESWQLAASGLSGVLGIPMDTGSHPLEAVDPEVKTFFADSLAAGDDWESPYP 60	Sequence 2, Appl1
39	1 MLFESWQLAASGLSGVLGIPMDTGSHPLEAVDPEVKTFFADSLAAGDDWESPYP 60	Sequence 2, Appl1
40	1 MLFESWQLAASGLSGVLGIPMDTGSHPLEAVDPEVKTFFADSLAAGDDWESPYP 60	Sequence 2, Appl1
41	1 MLFESWQLAASGLSGVLGIPMDTGSHPLEAVDPEVKTFFADSLAAGDDWESPYP 60	Sequence 2, Appl1
42	1 MLFESWQLAASGLSGVLGIPMDTGSHPLEAVDPEVKTFFADSLAAGDDWESPYP 60	Sequence 2, Appl1
43	1 MLFESWQLAASGLSGVLGIPMDTGSHPLEAVDPEVKTFFADSLAAGDDWESPYP 60	Sequence 2, Appl1
44	1 MLFESWQLAASGLSGVLGIPMDTGSHPLEAVDPEVKTFFADSLAAGDDWESPYP 60	Sequence 2, Appl1
45	1 MLFESWQLAASGLSGVLGIPMDTGSHPLEAVDPEVKTFFADSLAAGDDWESPYP 60	Sequence 2, Appl1

Db 241 TLRSTEGEDODLMDGDIHVNGQPMPELVNQPCKRYRRLNAAVSRAMLLYLVRITSSPNVR 300
QY IPFOVIASDAGLLQAPVQTSNLYLAVEREYIIIDFTNPAQOTLDLRNVAETNDVGDDE 360
Db 301 IPFOVIASDAGLLQAPVQTSNLYLAVEREYIIIDFTNPAQOTLDLRNVAETNDVGDDE 360
QY 361 YARLEVMRFVYSSGTVEDNSQVSTLRDVPFPKKEGPADKHKFEERSNGHYLLINDVGF 420
Db 361 YARLEVMRFVYSSGTVEDNSQVSTLRDVPFPKKEGPADKHKFEERSNGHYLLINDVGF 420
QY 421 ADVNERVLAKPELGVEWELENSGSGSHVPHILVDKILKRTGSGQVMPYESAGLK 480
Db 421 ADVNERVLAKPELGVEWELENSGSGSHVPHILVDKILKRTGSGQVMPYESAGLK 480
QY 481 DVVWLGREGTELTIEAHYQPMTGAYWMHCHNLIHEDNDMAAVFNVTAMEKGYLOEDFEDP 540
Db 481 DVVWLGREGTELTIEAHYQPMTGAYWMHCHNLIHEDNDMAAVFNVTAMEKGYLOEDFEDP 540
541 MNPKRRAVPYRNNDPHARAGNFSASITARVOELAEQEPYRNRLDEILDIGIEE 594
541 MNPKRRAVPYRNNDPHARAGNFSASITARVOELAEQEPYRNRLDEILDIGIEE 594

RESULT 2

US-10-080-210-2
; Sequence 2, Application US/10080210
; Patent No. US20020142423A1
; GENERAL INFORMATION:
; APPLICANT: Wang, Huaming
; APPLICANT: Bodie, Elizabeth A.
; TITLE OF INVENTION: Phenol Oxidizing Enzymes
; FILE REFERENCE: GC561-3
; CURRENT APPLICATION NUMBER: US/10/080,210
; CURRENT FILING DATE: 2002-02-19
; PRIOR APPLICATION NUMBER: US 09/720,871
; PRIOR FILING DATE: 1998-12-23
; PRIOR APPLICATION NUMBER: US 09/338,723
; PRIOR FILING DATE: 1999-06-23
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 594
; TYPE: PRT
; ORGANISM: Stachybotrys chartarum
US-10-080-210-2

Query Match 100.0%; Score 3189; DB 12; Length 594;

Best Local Similarity 100.0%; Pred. No. 2.6e-251; Mismatches 0; Indels 0; Gaps 0;

Matches 594; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
1 MLFMSWQLAASGLISGLVIGIPMDTGSHPRIEAVDPEVTEVFADSLAAAGDDMESPPY 60
1 MLFMSWQLAASGLISGLVIGIPMDTGSHPRIEAVDPEVTEVFADSLAAAGDDMESPPY 60
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Db 61 NLRYNALPIPPVKOPKMIITNPVTGKDITWYEIEIKFQOIRIYPTLRPATLVGDGKSP 120
QY 121 GPTFNVPRGTEVVRFINNATVENSVHLHGSRSRAPFDGMAEDVTFPEGYKDYFFPNYOS 180
Db 121 GPTFNVPRGTEVVRFINNATVENSVHLHGSRSRAPFDGMAEDVTFPEGYKDYFFPNYOS 180
QY 181 ARLLMYHDHAFMKTAEKNYFGQAGAYIINDAEADALGIPSGYGEEDIPLLITAKYYNDG 240
Db 181 ARLLMYHDHAFMKTAEKNYFGQAGAYIINDAEADALGIPSGYGEEDIPLLITAKYYNDG 240
QY 241 TLRSTEGEDODLMDGDIHVNGQPMPELVNQPCKRYRRLNAAVSRAMLLYLVRITSSPNVR 300
Db 241 TLRSTEGEDODLMDGDIHVNGQPMPELVNQPCKRYRRLNAAVSRAMLLYLVRITSSPNVR 300
QY 301 IPFOVIASDAGLLQAPVQTSNLYLAVEREYIIIDFTNPAQOTLDLRNVAETNDVGDDE 360
Db 301 IPFOVIASDAGLLQAPVQTSNLYLAVEREYIIIDFTNPAQOTLDLRNVAETNDVGDDE 360

QY 361 YARLEVMRFVYSSGTVEDNSQVSTLRDVPFPKKEGPADKHKFEERSNGHYLLINDVGF 420
Db 361 YARLEVMRFVYSSGTVEDNSQVSTLRDVPFPKKEGPADKHKFEERSNGHYLLINDVGF 420
QY 421 ADVNERVLAKPELGVEWELENSGSGSHVPHILVDKILKRTGSGQVMPYESAGLK 480
Db 421 ADVNERVLAKPELGVEWELENSGSGSHVPHILVDKILKRTGSGQVMPYESAGLK 480
QY 481 DVVWLGREGTELTIEAHYQPMTGAYWMHCHNLIHEDNDMAAVFNVTAMEKGYLOEDFEDP 540
Db 481 DVVWLGREGTELTIEAHYQPMTGAYWMHCHNLIHEDNDMAAVFNVTAMEKGYLOEDFEDP 540
541 MNPKRRAVPYRNNDPHARAGNFSASITARVOELAEQEPYRNRLDEILDIGIEE 594
541 MNPKRRAVPYRNNDPHARAGNFSASITARVOELAEQEPYRNRLDEILDIGIEE 594

RESULT 3

US-10-080-233-2
; Sequence 2, Application US/10080233
; Patent No. US20020151450A1
; GENERAL INFORMATION:
; APPLICANT: Wang, Huaming
; TITLE OF INVENTION: No. US20020151450A1 Phenol Oxidizing Enzymes
; FILE REFERENCE: GC567
; CURRENT APPLICATION NUMBER: US/10/080,233
; CURRENT FILING DATE: 2002-02-19
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 594
; TYPE: PRT
; ORGANISM: Stachybotrys sp.
US-10-080-233-2

Query Match 100.0%; Score 3189; DB 12; Length 594;

Best Local Similarity 100.0%; Pred. No. 2.6e-251; Mismatches 0; Indels 0; Gaps 0;

Matches 594; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
1 MLFMSWQLAASGLISGLVIGIPMDTGSHPRIEAVDPEVTEVFADSLAAAGDDMESPPY 60
1 MLFMSWQLAASGLISGLVIGIPMDTGSHPRIEAVDPEVTEVFADSLAAAGDDMESPPY 60
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Db 61 NLRYNALPIPPVKOPKMIITNPVTGKDITWYEIEIKFQOIRIYPTLRPATLVGDGKSP 120
QY 121 GPTFNVPRGTEVVRFINNATVENSVHLHGSRSRAPFDGMAEDVTFPEGYKDYFFPNYOS 180
Db 121 GPTFNVPRGTEVVRFINNATVENSVHLHGSRSRAPFDGMAEDVTFPEGYKDYFFPNYOS 180
QY 181 ARLLMYHDHAFMKTAEKNYFGQAGAYIINDAEADALGIPSGYGEEDIPLLITAKYYNDG 240
Db 181 ARLLMYHDHAFMKTAEKNYFGQAGAYIINDAEADALGIPSGYGEEDIPLLITAKYYNDG 240
QY 241 TLRSTEGEDODLMDGDIHVNGQPMPELVNQPCKRYRRLNAAVSRAMLLYLVRITSSPNVR 300
Db 241 TLRSTEGEDODLMDGDIHVNGQPMPELVNQPCKRYRRLNAAVSRAMLLYLVRITSSPNVR 300
QY 301 IPFOVIASDAGLLQAPVQTSNLYLAVEREYIIIDFTNPAQOTLDLRNVAETNDVGDDE 360
Db 301 IPFOVIASDAGLLQAPVQTSNLYLAVEREYIIIDFTNPAQOTLDLRNVAETNDVGDDE 360
QY 361 YARLEVMRFVYSSGTVEDNSQVSTLRDVPFPKKEGPADKHKFEERSNGHYLLINDVGF 420
Db 361 YARLEVMRFVYSSGTVEDNSQVSTLRDVPFPKKEGPADKHKFEERSNGHYLLINDVGF 420
QY 421 ADVNERVLAKPELGVEWELENSGSGSHVPHILVDKILKRTGSGQVMPYESAGLK 480
Db 421 ADVNERVLAKPELGVEWELENSGSGSHVPHILVDKILKRTGSGQVMPYESAGLK 480
QY 481 DVVWLGREGTELTIEAHYQPMTGAYWMHCHNLIHEDNDMAAVFNVTAMEKGYLOEDFEDP 540
Db 481 DVVWLGREGTELTIEAHYQPMTGAYWMHCHNLIHEDNDMAAVFNVTAMEKGYLOEDFEDP 540

|||||
Db 481 DVVWLGREGTLLTEAHQPTWGAYMWHCHNLHEDNDMAVFNVTAMEKGVLQDFEDP 540
Qy 541 MNPWRVAVPNRNDFHARAGNFSASTARVOELAEOPRYRLDEILLDIGEE 594
Db 541 MNPWRVAVPNRNDFHARAGNFSASTARVOELAEOPRYRLDEILLDIGEE 594
RESULT 4
US-09-338-723A-4
; Sequence 4, Application US/09338723A
; Patent No. US2002019038A1
; GENERAL INFORMATION:
; APPLICANT: Huang, Wang
; TITLE OF INVENTION: Phenol Oxidizing Enzymes
; FILE REFERENCE: GC561-2
; CURRENT APPLICATION NUMBER: US/09/338, 723A
; PRIOR FILING DATE: 1999-06-23
; PRIOR APPLICATION NUMBER: 09/220, 871
; PRIOR FILING DATE: 1998-12-23
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 4
; LENGTH: 627
; TYPE: PRF
; ORGANISM: Bipolaris spicifera
US-09-338-723A-4

Query Match 61.3%; Score 1954.5; DB 10; Length 627;
Best Local Similarity 61.1%; Pred. No. 9e-151;
Matches 367; Conservative 79; Mismatches 134; Indels 21; Gaps 8;

Qy 2 LFKSMOLAAAGSLGSLGIVGIPMDTGSHPTEAVDEPKTEVPADSLAAAGD----- 53
Db 6 LFSALQVLS---IAKGIYVAL--SERPAKEVDNTPDEKAA--LASIVEDDPADVYNNL 58
Qy 54 -DMESPYNLLRYNALPIPPVOKPMITNPYTGKDIWYEIEIKPFOQRIYPTLRPATL 112
Db 59 KMQSPREYLIIRPLRPIPAKEPNK-LNPVTNKEIWEYELIKPFOQVYPSLRPARL 117
Qy 113 VGTGMSGPTTNNPRGTEIVYRFINNAATVENSVAHLGSPSRAPFDGMAEDVTFPEEKD 172
Db 118 VGTGDISPPTIIVPRGTEAVVRFINOGDRESSIHLGSPSRAPFDGMAEDVIMKEGYD 177
Qy 173 YEPNVSARLLMYHDHAFMKTAEVAYFGAGAYIINDAEADALGSPGGEFDPLIT 232
Db 178 YTPNNQARFLMYHDHAFMKTAEVAYFGAGAYITDPAEDALGSPGGEYKIDPLVLS 237
Qy 233 AKYVADGTLRSTEGEDQDLMDGVYHNGQPMPLNVOPRYRFRFLNAASRAWLILYV 292
Db 238 SKYVADGTLKTSVGEDKSVMGDIHVNQOPMPLNVPRKRYRLFLNAASRAWLILYV 297
Qy 293 RTSSPNVRIPEOVYIASDAGLLQAPVQISNLYLAVEREYIIDFTNFAQOTLDLRVAET 352
Db 298 KQDNATRIPLPEOVYIASDAGLLTHPVQTSMDYAAERYEIVDFAPYAGQOTLDLRNFAKA 357
Qy 353 NDVGDEDEXTARLEVRVAVSSGTVEDNSOVPTLRDVPFRPKRGPAKHKFEERSNGH 412
Db 358 NGIGTDDYANTDKVARKFRVSSQTVYDVSVPBQLSQIOFPADKT-DIDHHRFRHTNGB 416
Qy 413 YLINDVGFADVNERVLAPELGTVEVWELENSSGMSHPVHILVDKILKRTGGRG-- 470
Db 417 WRINGIGFADVNERVLAKEVPGTVELMELENSSGMSHPVHILVDKILKRTGGRG-- 476
Qy 471 VMPYRAGLKVYVWLGRGTELLTEAHYQPTWGAYMWHCHNLHEDNDMAVFNVTAMEEK 530
Db 477 VMPYRAGLKVYVWLGRGTELLTEAHYQPTWGAYMWHCHNLHEDNDMAVFNVTAMEEK 536
Qy 531 GYLO-EDFEDPMNPKRAVYPNNDFHARAGNFSASTARVOELAEOPRYRLDEILL 589
Db 537 GYNETTDFHDPEDPMNSARPTAGDLTARSGLTFSEESIRARVNELEAOPYSIELAQVYAS 596
Qy 590 L 590

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Db 597 L 597
RESULT 5
US-10-080-210-4
; Sequence 4, Application US/10080210
; Patent No. US20020142423A1
; GENERAL INFORMATION:
; APPLICANT: Wang, Huang
; APPLICANT: Bodie, Elizabeth A.
; TITLE OF INVENTION: Phenol Oxidizing Enzymes
; FILE REFERENCE: GC561-3
; CURRENT APPLICATION NUMBER: US/10/080, 210
; PRIOR FILING DATE: 2002-02-19
; PRIOR APPLICATION NUMBER: US 09/220, 871
; PRIOR FILING DATE: 1998-12-23
; PRIOR APPLICATION NUMBER: US 09/338, 723
; PRIOR FILING DATE: 1999-06-23
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 627
; TYPE: PRF
; ORGANISM: Bipolaris spicifera
US-10-080-210-4

Query Match 61.3%; Score 1954.5; DB 12; Length 627;
Best Local Similarity 61.1%; Pred. No. 9e-151;
Matches 367; Conservative 79; Mismatches 134; Indels 21; Gaps 8;

Qy 2 LFKSMOLAAAGSLGSLGIVGIPMDTGSHPTEAVDEPKTEVPADSLAAAGD----- 53
Db 6 LFSALQVLS---IAKGIYVAL--SERPAKEVDNTPDEKAA--LASIVEDDPADVYNNL 58
Qy 54 -DMESPYNLLRYNALPIPPVOKPMITNPYTGKDIWYEIEIKPFOQRIYPTLRPATL 112
Db 59 KMQSPREYLIIRPLRPIPAKEPNK-LNPVTNKEIWEYELIKPFOQVYPSLRPARL 117
Qy 113 VGTGMSGPTTNNPRGTEIVYRFINNAATVENSVAHLGSPSRAPFDGMAEDVTFPEEKD 172
Db 118 VGTGDISPPTIIVPRGTEAVVRFINOGDRESSIHLGSPSRAPFDGMAEDVIMKEGYD 177
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Db 238 SKYVADGTLKTSVGEDKSVMGDIHVNQOPMPLNVPRKRYRLFLNAASRAWLILYV 297
Qy 293 RTSSPNVRIPEOVYIASDAGLLQAPVQISNLYLAVEREYIIDFTNFAQOTLDLRVAET 352
Db 298 KQDNATRIPLPEOVYIASDAGLLTHPVQTSMDYAAERYEIVDFAPYAGQOTLDLRNFAKA 357
Qy 353 NDVGDEDEXTARLEVRVAVSSGTVEDNSOVPTLRDVPFRPKRGPAKHKFEERSNGH 412
Db 358 NGIGTDDYANTDKVARKFRVSSQTVYDVSVPBQLSQIOFPADKT-DIDHHRFRHTNGB 416
Qy 413 YLINDVGFADVNERVLAPELGTVEVWELENSSGMSHPVHILVDKILKRTGGRG-- 470
Db 417 WRINGIGFADVNERVLAKEVPGTVELMELENSSGMSHPVHILVDKILKRTGGRG-- 476
Qy 471 VMPYRAGLKVYVWLGRGTELLTEAHYQPTWGAYMWHCHNLHEDNDMAVFNVTAMEEK 530
Db 477 VMPYRAGLKVYVWLGRGTELLTEAHYQPTWGAYMWHCHNLHEDNDMAVFNVTAMEEK 536
Qy 531 GYLO-EDFEDPMNPKRAVYPNNDFHARAGNFSASTARVOELAEOPRYRLDEILL 589
Db 537 GYNETTDFHDPEDPMNSARPTAGDLTARSGLTFSEESIRARVNELEAOPYSIELAQVYAS 596
Qy 590 L 590

Db 597 L 597

RESULT 6
US-10-080-210-7
; Sequence 7, Application US/10080210
; Patent No. US20020142423A1
; GENERAL INFORMATION:
; APPLICANT: Wang, Huaming
; APPLICANT: Bodie, Elizabeth A.
; TITLE OF INVENTION: Phenol Oxidizing Enzymes
; FILE REFERENCE: GC561-3
; CURRENT APPLICATION NUMBER: US/10/080,210
; PRIORITY FILING DATE: 2002-02-19
; PRIORITY FILING DATE: 1998-12-23
; PRIOR APPLICATION NUMBER: US 09/338,723
; PRIORITY FILING DATE: 1999-06-23
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: FastSeq for Windows Version 4.0
EQ ID NO 7
LENGTH: 627
TYPE: PRT
; ORGANISM: Curvularia pallescens
US-10-080-210-7

Query Match 60.5%; Score 1929.5; DB 12; Length 627;
Best Local Similarity 60.5%; Pred. No. 9.7e-149;
Matches 364; Conservative 81; Mismatches 134; Indels 23; Gaps 9;

2 LFKSMOLAAAGSLGSGVIGIPMDGSHPIEAVDEPVKTEVADSLAAGD----- 53
6 LFSMLQALAS--LAKGIVGAL--SERPAKIDETPDEKAA--LAAIVEDPADVETIL 58
54 -DMSPPYLLRYNALPIPVKOPKMITNPVTGKDIWYELIEIKFOQRIYPTLPATL 112
59 KDMSPPEPLIFREALPIPAKEPNK-MTNVPTNKEIYELIVIKPFNOYVPSLRARL 117
113 VGYGMSGPPFPNPRGTEYVRFINNATVENSYHLGSPSRAPDGAEDVTPPEKYD 172
118 VGYGDISPGPIIYPRGTEAVRVNNOGDRSSIHLSHSPSRAPDGAEDLIMKGPKD 177
173 YFPNYSARLLMYHDHAFMKTAENAYFGAGAYIINDEADALGPSGGEFDIPLT 232
178 YYYNNQAARLMTYHDHAFMKTAENAYFGAGAYIINDEADALGPSGGEFDIPLT 237
233 AKYNNADGTLSTEGEDODIMGDIYHNGQWPFLNVOPRKXRFRLNAAVSRAMLTYL 292
238 SKFYNSDGLTQTSVGEDNSLWGDYIHVNGQWPFLNVOPRKXRFRLNAAVSRAMLTYL 297
293 RTSSPNRIPPOVYASDAGLLQAPVQTSNLYLAVEREITIDTFNAGOTLDIRNAET 352
298 KQQTATRLPQVYASDAGLLQAPVQTSNLYLAVEREITIDTFNAGOTLDIRNAET 357
353 NDVDEDEYARTLEVMRFVSSGTVEDNSQVPTSLRDVPPPKRKGPAKHKFKERSNGH 412
358 NGVETDDDYANTDKYVMAFHYSSQAVYDVSYPADLSQIQFADKTG-IDHFRHRTISE 416
413 YLINDVGFADVNERVLAKPELGTVEVWELNENSGGWSHPVHILVDFEILKRTGG--RG 469
417 WRINGIGFADYONRILAKVPRGTVEWELNENSGGWSHPVHILVDFEIVARYGDESRG 476
470 QWMPYESAGLKDYVVLGRGETLTLEAHYQPTGAYMMHCHNLIHEDNDMAAVNTAMEE 529
477 -VMYESAGLKDYVVLGRGETLTLEAHYQPTGAYMMHCHNLIHEDNDMAAVNTAMEE 535
530 KGYLQ-EDFEDPMNPKRAVYNNRNDHARAGNSASITARVOELAEQEPYNDLELE 588
536 FGNHETTFDHPEDSRMSARPFADLTARSGITSEASIRARVNELAEQEPYSELADYTA 595
589 DL 590
596 SL 597

Db 597 L 597

RESULT 7
US-09-942-185-4
; Sequence 4, Application US/09942185
; Patent No. US20020165113A1
; GENERAL INFORMATION:
; APPLICANT: Aehle, Wolfgang
; APPLICANT: Convents, Daniel
; APPLICANT: Doornink, Monique
; APPLICANT: van Gastel, Frans
; APPLICANT: Rodrigues, Ana
; APPLICANT: Topozada, Amr
; APPLICANT: De Vries, Cornelis Hendrikus
; APPLICANT: Wang, Huaming
; TITLE OF INVENTION: Detergent Compositions Comprising No. US20020165113A1 Phenol
; FILE REFERENCE: C7567
; CURRENT APPLICATION NUMBER: US/09/942,185
; PRIORITY FILING DATE: 2001-08-29
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: FastSeq for Windows Version 4.0
EQ ID NO 4
LENGTH: 572
TYPE: PRT
; ORGANISM: Myrothecium verucaria
US-09-942-185-4

Query Match 54.1%; Score 1724.5; DB 9; Length 572;
Best Local Similarity 60.3%; Pred. No. 4.2e-132;
Matches 322; Conservative 75; Mismatches 128; Indels 9; Gaps 7;

57 SPPYLLRYNALPIPVKOPKMITNPVTGKDIWYELIEIKFOQRIYPTLPATLVGYD 116
43 SPOYP-METVPLRPVYVQPRLTVTNPNVNGEIMYVEIETPHQVYPDGSDALVGYD 101
117 GMSGPPFPNPRGTEYVRFINNATVENSYHLGSPSRAPDGAEDVTPPEKYD 176
102 GMSGPPFPNPRGTEYVRFINNATVENSYHLGSPSRAPDGAEDVTPPEKYD 161
177 NYQARLLMYHDHAFMKTAENAYFGAGAYIINDEADALGPSGGEFDIPLTLYKXY 236
162 NRQARLLMYHDHAFMKTAENAYFGAGAYIINDEADALGPSGGEFDIPLTLYKXY 221
237 NADGTLSTEGEDODIMGDIYHNGQWPFLNVOPRKXRFRLNAAVSRAMLTYL 296
222 TANGLVYTTNGLNLSFWGDYIHVNGQWPFLNVOPRKXRFRLNAAVSRAMLTYL 281
297 PNVRIPPOVYASDAGLLQAPVQTSNLYLAVEREITIDTFNAGOTLDIRNAET 355
282 IDTRLPRVYASDAGLLQAPVQTSNLYLAVEREITIDTFNAGOTLDIRNAET 341
356 GDEDEYARTLEVMRFVSSGTVEDNSQVPTSLRDVPPPKRKGPAKHKFKERSNGH 413
342 GTDIDYDNTOKVMAFHYSSQAVYDVSYPADLSQIQFADKTG-IDHFRHRTISE 399
414 LINDVGFADVNERVLAKPELGTVEVWELNENSGGWSHPVHILVDFEILKRTGG--QV 471
400 TINGVADYONRILAKVPRGTVEWELNENSGGWSHPVHILVDFEIVARYGDESRG 459
472 MPYSSAGLKDYVVLGRGETLTLEAHYQPTGAYMMHCHNLIHEDNDMAAVNTAMEE 531
460 MPYSS-GLKDYVVLGRGETLTLEAHYQPTGAYMMHCHNLIHEDNDMAAVNTAMEE 518
532 YLQDEDEYARTLEVMRFVSSGTVEDNSQVPTSLRDVPPPKRKGPAKHKFKERSNGH 585
519 YNATVYDPMKELMQRARPYELGEGQASQGSQVAVYERIQTMAYRYAADA 572

RESULT 8
US-09-942-185-2
; Sequence 2, Application US/09942185
; Patent No. US20020165113A1
; GENERAL INFORMATION:

Query Match	53.88;	Score 1716.5;	DB 9;	Length 583;
Best Local Similarity	61.08;	Pred. No. 1.9e-131;		
Matches 330;	Conservative 67;	Mismatches 125;	Indels 19;	Gaps 9

	APPLICANT:	Janssen, Giselle G.	
	APPLICANT:	Murray, Christopher J.	
	APPLICANT:	Wang, Huaming	
	APPLICANT:	Minetzký, Deborah S.	
	TITLE OF INVENTION:	Binding Phenol Oxidizing Enzyme-peptide	
	TITLE OF INVENTION:	Complexes	
	FILE REFERENCE:	GC690	
	CURRENT APPLICATION NUMBER:	US/09/954,385	
	CURRENT FILING DATE:	2001-09-12	
	NUMBER OF SEQ ID NOS:	433	
	SOFTWARE:	FastSeq for Windows Version 4.0	
	SEQ ID NO 1		
	LENGTH:	583	
	TYPE:	PRT	
	ORGANISM:	Stachybotrys chartarum	
	US-09-954-385-1		
Query Match	53.8%	Score 1716.5:	DB 9; Length 583;
Best Local Similarity	61.0%;	Pred. No.19e-131;	
Matches 330;	Conservative 67;	Mismatches 125;	Indels 19; Gaps .9;
QY	57	SPPNLLRYRALPIRPYPKOPRMITTNVPTGKDVIYEIEIKFOORTIPLTPRLATLYGD	116
Db	45	SPEPL-ALEYELPRLPIPKAPR-TYPRNNTGSDILYEMEIRPFHQOIVPDLEPANMGYD	102
QY	117	GMSGPFPFNVPKGTETVYRFLTNN--TVENSVLHGSFRAFPFGMAEDVTFFPGBYKDY	174
Db	103	GMSGCPITIVPGRGESVYRFVNSGENTSPPNSVHLHGFSRAPFGMAEDTTQPGEYKDY	162
QY	175	PFPNOSARLIMYHDHAMAKTAENMYFPOAGAYIINDAEADMLGLPSGGEFDIFLLITAK	234
Db	163	YPNQAQRMLMTHDHAMSTIAENNAVMGOAGYIMIDDPREDALNLPSGTGEFDITPLVLTAK	222
QY	235	YYNADGTLRSTEGEDODLMDGVIVHNGQPMFPLNVOPRKYFRFLNAAVSRAWLLYLVRT	294
Db	223	RYNADGTLFTNGEVSSEFMGDIYOVNQPMFMLNVOPRKYFRFLNAAVSRSFALYTATS	282
QY	295	SSPNVRIPFQVIASDAGLLQAPVOTSNLYLAVEREYELLIDFTNPAGOTLDLRNVAETND	354
Db	283	EDESTRLPFQVIADGGILLEGPVDITDLISMAERMEVYIDFSFAGOSIDIRMLPGADG	342
QY	355	VGDEDEARLEVEWRFVYSSTGE--DNSQVPSLTRVPRPHKEG----PA----DKHF	404
Db	343	LGEPPERDNTDKVWRPFVYDE-VLESPTSISEPAMLRDVPF--EGGMWDPRANPTDDTE	398
QY	405	KFERSNGHYLLINDGFADVNERVYLAKEDELCTVEWELENSSGSGSHPRHIHLVDFKILKR	464
Db	399	TFGANGQMWTINGTTFSDVENKRLLRNPRDVTELWRELENNNGMTHPRHITLVDFRVLSR	458
QY	465	TGGRGQMPYESAGLKDVVWLIGRGETILLTEAHQWPMTGAVYMHCHNLIHEDNDMMAAENV	524
Db	459	STARNG-VEPYEAAGLKOVVWMLAREVVYVEAHYAPFGVYMLHCHNLIHEDHDMMAENV	517
QY	525	TAMEEKYILOEDFEDPMNPKRAVPRYNRDNFHAAGNFSAESTARVOELAEODEPRYRLD	584
Db	518	TVLGDIYGYNTETFIDPMEPLMRPRPFLLEGRENSSGFSSELAIIDRILOEMASFNPYQAD	577
QY	585	E 585	
Db	578	D 578	
<hr/>			
RESULT 10			
US-10-080-233-4			
Sequence 4, Application US/10080233			
Patent No. US20020151450A1			
GENERAL INFORMATION:			
APPLICANT: Wang, Huaming			
TITLE OF INVENTION: No. US20020151450A1el Phenol Oxidizing Enzymes			
FILE REFERENCE: GC567			
CURRENT APPLICATION NUMBER: US/10/080,233			
CURRENT FILING DATE: 2002-02-19			
NUMBER OF SEQ ID NOS: 5			

QY 414 LINDVGFADYNERVYLAKELGTEVWELENSGSHPHVHLVDKILKRTGRC--QV 471
DB 400 TINGAFADYONRLNAPVGTVERWELINAGNWTHTIHLVDFKVSFTSGNNARTV 459
QY 472 MPYESAGLKDYVWLGRTGTEAHYOPWTGAYMMHCHNLTHEDDMAVFNVTAMEEG 531
DB 460 MPYES-GKADYVWLGRTGTEAHYOPWTGAYMMHCHNLTHEDDMAVFNVTAMEEG 518
QY 532 YLQEDFEDPMNPKRAVYNNRNDPFAHAGNSAESITARVOELAQDEPYNRLDE 585
DB 519 YNAFVFDPMNEELMQARPELGEFGQSGFSVQAVTERIQTMATRYNAADE 572

RESULT 2
F69604
spore coat protein (outer) cota - Bacillus subtilis
C:Species: Bacillus subtilis
C:Date: 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 15-Oct-1999
C:Accession: F69604; A27393; S02538
A:Authors: F. Ogatawara, N. Moser, I. Albertini, A.M. Alloni, G. Azevedo, V. Bertez
Bron, S.; Brouillet, S.; Brusch, C.V.; Caldwell, B.; Capuano, V.; Carter, N.M.; Chd
Ehrlich, S.D.; Emerson, P.T.; Entlan, K.D.; Errington, J.; Fabret, C.; Ferrati, E.
Kunze, J.; Harwood, C.R.; Henaut, A.; Hillbert, H.; Holsappel, S.; Hosono, S.; Hullo, M.F.
Kocher, P.; Koningstein, G.; Krogh, S.; Kumano, M.; Kunita, K.; Lapidus, A.; Lardinis,
A.; Lauber, J.; Lazarevic, V.; Lee, S.M.; Levine, A.; Liu, H.; Masuda, S.; Maueel
Y, M.; Ogawa, K.; Ogilwara, A.; Oudaga, S.H.; Parro, V.; Pohl, T.M.; Portetelie
Rieger, M.; Rivolta, C.; Rocha, E.; Roche, B.; Rose, M.; Sadale, Y.; Sato, T.; Scanlon,
A.; Schleich, S.; Schaefer, R.; Scoffone, F.; Sekiguchi, J.; Sekowska, A.; Senot
akeuchi, M.; Tamakoshi, A.; Tanaka, T.; Tarpstra, P.; Togonni, A.; Tosato, V.; Uchiyama,
T.; Winters, P.; Wipat, A.; Yamamoto, H.; Yamane, K.; Yasumoto, K.; Yata, K.; Yoshida, K.
A:Authors: Yoshikawa, H.F.; Zumbstein, E.; Yoshikawa, H.; Danchin, A.
A:Title: The complete genome sequence of the Gram-positive bacterium Bacillus subtilis.
A:Reference number: A69580; MUID:98044033; PMID:9384377
A:Accession: F69604
A:Status: preliminary; nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-513 <KUN>
A:Cross-references: GB:259107; GB:AL009126; NID:92632866; PIDN:CAB12449.1; PID:el182609;
A:Experimental source: strain 168
J:Donovan, W.; Zheng, L.; Sandman, K.; Losick, R.
J: Mol. Biol. 196, 1-10, 1987
A:Title: Genes encoding spore coat polypeptides from Bacillus subtilis.
A:Reference number: A27393; MUID:86011308; PMID:2821284
A:Accession: A27393
A:Status: not compared with conceptual translation
A:Molecule type: DNA
A:Residues: 1-37 <DON>
A:Authors: Sandman, K.; Kroos, L.; Cutting, S.; Youngman, P.; Losick, R.
J: Mol. Biol. 200, 461-473, 1988
A:Title: Identification of the promoter for a spore coat protein gene in Bacillus subtilis
A:Reference number: S02538; MUID:88286730; PMID:3135411
A:Accession: S02538
A:Status: not compared with conceptual translation
A:Molecule type: DNA
A:Residues: 1-32 <SAN>
C:Comment: this spore coat protein is responsible for the characteristic brown pigment c
A:Genetics:
A:Gene: cota; pilg
C:Keywords: sporulation

Query Match 22.4%; Score 713; DB 2; Length 513;
Best Local Similarity 34.6%; Pred. No. 2e-46;
Matches 183; Conservative 75; Mismatches 175; Indels 96; Gaps 18;

QY 66 NALPFP-----PVKOPKMIITNPVYKDIWYEIEIKFOQRIYPTLRPAVLVGDGSPG 121
DB 8 DALPFPITLKPVOO-----SKETTYEVMECTYQHLHDLDPPTLRMGNGLEPG 57
QY 122 PTENVPRGTETVAFINNA-----TVENS-----VHLHSGSPRAPDPG 159
DB 58 PTIEVKKNENVYKMMNNLSTHFLP IDHTIHSDSHPEPEYKTVVHHLGGVTPDDSDG 117

QY 160 MAE-----DYTPPEGY-----KDYFPNYSARLLMYTHDAFMKTANAFGAGAYIINDE 211
DB 118 YPEAMFSNDFEOTGTYFFKREYVHYHNOQRGALWTHDHAMALITRLNVTAGLVAYIITDP 177
QY 212 AEDALGDSGYGEEDIPILITAKYNNADGTL--RSTEGEDDL-----MGDVIHY 259
DB 178 KEKRLKPS--DEYDVPILITDRITNEDGSLFPYAPAPENPSPSPSPSPSPSPSPSPSPSP 235
QY 260 NGQPPPLNVPQKRFREFLNAAVSRALVLYVRSNNRNPFPVYASDGLQAPQT 319
DB 236 NGKVPYLEVEPRKTRFENYASNTNTNLSLNDGCD-----FLQISDGLLPRSKL 289
QY 320 SNLYLVAERYEIIIDTFNFAQOTDLRNVAET--NDVDEDEYARTLEVMFVSSGYVE 378
DB 290 NSFSLAPARERDIIIDTFAYEGESIIILANSAGCGDVAPEND-----ANIMGFRTKPLAQ 345
QY 379 -DNSQVSTLADVPPPKKEGPADKHEFFERSNGHY-----LINDVGFADYNERVYLAKPE 432
DB 346 KDESRRKPKYLYASYPEVQHERIONITRTLACTODEYGRVLLNNKRWMD--PVTERPK 402
QY 433 LGTYVWELENSGSHPHVHLVDKILKRTGRC--QV 471
DB 403 VGTETWMSIINPTKG--THPHDLVSEVYLRPPDIARYOESGELSTGPAVPPPESEK 461
QY 477 AGLDVWLGRTGTEAHYOPWTGAYMMHCHNLTHEDDMAVFNVT 525
DB 462 -GKMDTIOAHAGEVLRATGPGSGRYVMCHLHEDDYMMRMDIT 509

RESULT 3
B86364
hypothetical protein F19G10.5 - Arabidopsis thaliana
C:Species: Arabidopsis thaliana (mouse-ear cress)
C:Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 31-Dec-2001
C:Accession: B86364
A:Authors: A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alon
Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar,
ansen, N.F.; Hughes, B.; Huzar, L.
Nature 408, 816-820, 2000
A:Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim,
C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marzia
Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
A:Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallo
ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.
A:Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.
A:Reference number: A86411; MUID:21016719; PMID:11130712
A:Accession: B86364
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-568 <STO>
A:Cross-references: GB:AB051172; NID:92462832; PIDN:AB72167.1; GSPDB:GN00141
C:Genetics:
A:Map position: 1

Query Match 15.1%; Score 480; DB 2; Length 568;
Best Local Similarity 28.0%; Pred. No. 1.4e-28;
Matches 146; Conservative 78; Mismatches 167; Indels 130; Gaps 20;

QY 109 PATLVGVDGMS-----PGTFNVPRTGTEVYVRRIN-----AT-----V 142
DB 71 PATVPAVGTGSRSAATVPGTITETVYGVVDVYVWRNHLPSKSHLPMDPTISPAPKRGGI 130
QY 143 ENSVHLGSPSRAPFDGMAEDVPPGKYKD-----YFPPYQASARLLMYTHDAFMK 193
DB 131 PTYVHLHGGIHEPISDGN--DAMTAFKRETRGPMYTTITLHYEKKQOPGMWYTHDHAMGL 189
QY 194 TAENAVFGAGAYIINDEA-EDALGDSGYGEEDIPILITAKYNNADGTL--RSTEGEDDL 251
DB 190 TRVNLGAGLVAGAYILRHAAVESPPQLPTG--DEFDRPLIIPDRSPKRGSIYMATGNPS 248
QY 252 L-----MGDYHVGQVPPPLNVPQKRFREFLNAAVSRALVLYVRSNNRNPFPVYASDGLQAPQT 319

Db 249 IHPQOPEYEGDYIIVNGKAMPRLNRRKRYRRIINASNAREFFKFF-----SNGLDF 302
OY 304 QVYASAGLLQAVQTSNLYLAVEREIIIDFTNAGQPLDLRNA-----ETNDYGD 358
Db 303 IIVGSSAYLSKPVKRSKILLSPSEIVDVYDEPKSPSRVLANDPYPSGDPAE 362
OY 359 DEYARTLEVARFVYSGTVDNSQVSTLRDVPFPKRGADKHEFER--SNG-----H 412
Db 363 NG-----KVMKFIINSEEDDTCTIKKLINYNADVSNVLTIRYSMEYVNSDEPT 417
OY 413 YLINDYGF-ADVERVLAPELCTVEWELENSGGSHPHVHLVDKILKRTGGRQV 471
Db 418 IIVNGLPYEAQVTE-----PKSGTVEWEVINTLED-NHPLHILGLFKEVQTA----- 467
OY 472 MPYESGLKD-----VWLGREGELTIEAHOPTG----- 502
468 --LLAAGLEEFKECKMTRKQNDAYKQISKYARGKATATAEHMKVYKMPGHVTRILV 525
503 -----AYMWHCHNLIEDNDMAVFNV 524
526 RFSYIHTNMSYPPDPYQERGVYVCHLHEDMMMRPLKV 566

RESULT 4
G96734

Spore coat protein-like protein, 24980-21957 [imported] - Arabidopsis thaliana
C:Species: Arabidopsis thaliana (mouse ear cress)
C:Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 31-Mar-2001
C:Accession: G96734
R:Theologian, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso,
Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.;
ansen, N.F.; Hughes, B.; Hultzer, L.
Nature 408, 816-820, 2000
A:Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.
C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Malt, R.; Marziani,
Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
A:Authors: Salzberg, S.L.; Schwartz, J.R.; Shin, P.; Southwick, A.M.; Sun, H.; Tallon,
ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.
A:Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.
A:Reference number: A86141; M01D:21016719; PMID:11130712
A:Residues: 1-591 <STO>
A:Status: Preliminary
A:Accession: G96734
A:Molecule type: DNA
A:Residues: 1-591 <STO>
A:Cross-references: GB:AE005173; NID:g67141313; PIDN:AAF26006.1; GSPDB:GN00141
C:Genetics:
Gene: F23N20.3
Map position: 1

Query Match 14.1%; Score 450; DB 2; Length 591;

Best Local Similarity 27.4%; Pred. No. 2.9e-26;
Matches 142; Conservative 74; Mismatches 182; Indels 120; Gaps 18;

OY 109 PATLVGYDMS-----PGFTFNVPRGTETVVFVN-----NATV 142
Db 86 PATPVAYGTSKRSATVPGETIAYVGVDTYVWNRMLPLHLILPMDPTSPAIKKGCI 145
OY 143 ENSVHLHGSPSRAPFGMAEDVTFPGETKD-----YFPNYOSARILMTYHNAFMK 193
Db 146 PTVVHLHGGLHEPTSDGNA-DSWFTAGFKETGSKWKTKTTHYVKKOQPGMMVYHDAAGL 204
OY 194 TAENAYFGGAGAYII-NDKEDALGLPSGGEEDIPILITAKYNNADGTL-RSREGED-- 249
Db 205 TRVNLALGILGSIILKHSVESPLRLPTG-REFDRPLVITDRSFRKDGSIYMANNGNPT 263
OY 250 -----ODLMGDVYHNGQWPLVNOPRKRYRFRFLNAVSRAMLVLYVTSSPNVAF 303
Db 264 IHPQOPEYEGDYIIVNGKAMPRLNRRKRYRRIINASNAREFFKFF-----SNGLDF 317
OY 304 QVYASAGLLQAVQTSNLYLAVEREIIIDFTNAGQPLDLRNAETMDVGDDEYAR 363
Db 318 IIVGSSAYLSKPVKRSKILLSPSEIVDVYDEPKSPSRVLANDPYPSGDPAE 377

OY 364 TLEVARFVYSGTVDNSQVSTLRDVPFPKRGADKHEF--KFERNG-----HYLIN 416
Db 378 NSKMKRTIYKSSVDTSIIPKLELP-PAHYSTRTRKIANFEVSSIDEFTYLYIN 436
OY 417 DVGADVNERVLAPELCTVE-----VWELENSGGSHPHVHLVDKILKRTG 466
Db 437 GLPY--NAVTEPRKIGTSEFKSLMLTIKWEVINLTED-NHPLHILGLFVLEOTA 492
OY 467 -----GROVPEESAGLKDV-----W 484
Db 493 LVNSEEFIECMTRKNDAYKCEISKYARGKATATAEHMKVYKMPGHVTRILVRSY 552
OY 485 IGRGETLITFAHOPTGAYMWHCHNLIEDNDMAVFNV 522
Db 553 IHSNYSIFDAPQEP--GYVHCHLHEDMMMRPLKV 587

RESULT 5
C70397

periplasmic cell division protein (Sufi) - Aquifex aeolicus
C:Species: Aquifex aeolicus
C:Date: 08-May-1998 #sequence_revision 08-May-1998 #text_change 05-Nov-1999
C:Accession: C70397
R:Decker, G.; Warren, P.V.; Gaasterland, T.; Young, W.G.; Lenox, A.L.; Graham, D.E.
Nature 392, 353-358, 1998
A:Title: The complete genome of the hyperthermophilic bacterium Aquifex aeolicus.
A:Reference number: A70300; M01D:9819666; PMID:9537320
A:Accession: C70397
A:Status: preliminary; nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-527 <NO>
A:Cross-references: GB:AE00724; NID:g2963585; PIDN:AAC07157.1; PID:g2983586; GB:AE0
A:Experimental source: strain VFS
C:Genetics:
A:Gene: sufi

Query Match 13.8%; Score 439.5; DB 2; Length 527;

Best Local Similarity 30.1%; Pred. No. 1.6e-25;
Matches 147; Conservative 72; Mismatches 191; Indels 79; Gaps 21;

OY 98 PFOQRIYPLRPATLVGYDMS-----GPTFNVPRGTETVVFVNATVENS 146
Db 58 PDGGRVSIATKMTTLEVIIPKSDTMLVYEIDNEVNPVILRKQGTFSADYVNSGDSII 117
OY 147 HLHGSPSRAP--DGAEDVTFPGETKYDYFPNT---QSARILMTYHDAFMKTAENAYFG 201
Db 118 HWHG--FRAPMKSDGHPYVAVKDE--TYSVPETIIDRSQTYFHHPHGRTGYQYVG 173
OY 202 QAGAYIINDKEDAL--GLPSGGEEDIPILITAKYNNADGTLRSTGEODLMGDVYH 259
Db 174 LAGITIEDDEDLKOALDEYGVDTIDDKTDSGGQVLYNPMGMGMGFWGDTILV 233
OY 260 NGQWPLVNOPRKRYRFRFLNAVSRAMLVLYVTSSPNVRIPOVYASAGLLQAVQ 319
Db 234 NLPNPNMDVBERKIRRIILINGSNARYRLALLR---GNGRMKRWYVYGSGLLDPTKEV 290
OY 320 SNIYLAVEREIIIDFT-----NPAQOTLDL-----RNAETN--- 353
Db 291 NEILVAGGERIDILVDRDASVNDYIKLYNPHNLIGMIGMRGMGMGMGMGMGNM 350
OY 354 -DVG--DEDYARTLEVARFVYSGTVDNSQVSTLRDVPFPKRGADKHEFERSN 410
Db 351 MDGMADNSEF---EVEFRVYKDSAYDS-IPQRLSEVT-PLNTGAOVQRTTLGMR 404
OY 411 GHYLIN-----DVGA--RVLAPELCTVEWELENSGGSHPHVHLVDKIL 462
Db 405 IIVTINETMEWDGAYANQDINNPRVLEQNGVDVILEYVNTGMY-HPHNHGFOQV 463
OY 463 KRTGGRQVMPYESA--GLADVWVLGREGELTIE--AHQOPGTGAYMWHCHNLIEDND 517
Db 464 ERSIG-----PLRATIDGMDVYVAVMETVRIADVMSHRYNEHQIYLCHLHEDG 518

QY 518 MAAVENVTA 526
DB 519 MAAVENVTA 527

RESULT 6

AC0414
Probable exported protein YP03409 [imported] - Yersinia pestis (strain CO92)
C:Species: Yersinia pestis
C:Date: 02-Nov-2001 #sequence_revision 02-Nov-2001 #text_change 02-Nov-2001
C:Accession: AC0414
R:Parkhill, J.; Wren, B.W.; Thomson, N.R.; Tildall, R.W.; Holden, M.T.G.; Prentice, M.B.; deno-Farraga, A.M.; Chillingworth, T.; Cronin, A.; Davies, R.M.; Davis, P.; Dougan, G.; Li, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.; Whitehead, S.; Barrrell, Nature 413, 523-527, 2001
A:Title: Genome sequence of Yersinia pestis, the causative agent of plague.
A:Reference number: AB0001; MUID:21470413; PMID:11566360
A:Accession: AC0414
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-533 <KUR>
A:Cross-references: GB:AL590842; PIDN:CAC92639.1; PID:g15981336; GSPDB:GN00175
A:Gene: YP03409

Query Match 12.7%; Score 405.5; DB 2; Length 533;
Best Local Similarity 27.1%; Pred. No. 6.2e-23;
Matches 146; Conservative 57; Mismatches 217; Indels 119; Gaps 18;

QY 68 LPIPVKOPK---MITNPVTGKDIWYEIEIKPQORITPLRPATLV---GYDGMSPG 121
DB 34 LPIPLLPDANGKINLNIQISVWL-----PSTATQTMGYNLIG 76
QY 122 PTFNVPRGTETVFRINNATVENSVHLGSPSRAPFDGMAEDVTPPEGKYDYPNYOSA 181
DB 77 PAIRLRGKAVTIDITNLPEATVHMGLIEIPGVDGQALIGPKARKQTFVVEQPA 136
QY 182 RLWVHDAFMKTAENAFEGQAGATYINDEADALGSPGGEFDIPLITAKTYNADCT 241
DB 137 ATCWHPHRPHSKTGQVAMGLGLVLLIDSDSEIPLPRQMGVDDIPVILQDKLKHQ 196
QY 242 LRSTGEODL-----MGDIYHNGQWPPLVNOVRKY-RFRPLNAASRAMLYL 291
DB 197 V-----DYOLDVMTAAVGMFGDRMLTNGVPR-QQITPRGWRLRLNGCARSLNLAL 249
QY 292 VRTSSPNVRIPFOVIASDAGLQAPVQTSNLYLAVEREYIIIDTFNAGOTLDRNVAE 351
DB 250 -----SDGRPMYVIASDGLLAEPVYVRELPLMGERREVLVDTRD--GQSLDLVTLPV 301
QY 352 TNDVDEDEYARTLEVMEFVYSSGIVEDNSQV-PESTLDVPPPRKEGRADKHF----- 404
DB 302 TOMGNTLAPFDQPLFVLRIQPS--LAIGSOVLPESLVIVPELADVTGVOERFQJLMDP 358
QY 405 KEERSNGHYLI-----NDVGFAD----- 422
DB 359 KLDMLGQALVARIYGMKAMGMNMGDMGANDHGNRDMSCGKKKMGDHTMGCAPAFN 418
QY 423 -----VNERVLAKE-----LGTVEVWELENSSGSHPVHILVDFKILKRTGGRQ 470
DB 419 FSHNRINGKAFSMTPEPAFAKQKYEKWTISGEGDMLHPRHVGTQFRILTEG----- 474
QY 471 VMPPE-SAGLKDVMWL--GRGETLTIEAHYQPTGAYVMHCHNLIHEDNDMAVENVTA 526
DB 475 KPPAEHRGRKMDIVAVEGARSEILVRFNYLAPASTPYMAHCHLHEHEDTGMMLGPTVSA 533

RESULT 7

AC3582
Probable blue-copper protein yack precursor [imported] - Brucella melitensis (strain 16M)
C:Species: Brucella melitensis
C:Date: 01-Feb-2002 #sequence_revision 01-Feb-2002 #text_change 01-Feb-2002
C:Accession: AC3582
R:DelVecchio, V.G.; Kapratral, V.; Redkar, R.J.; Patra, G.; Mijer, C.; Los, T.; Ivanova,

; Mazur, M.; Goldsman, E.; Selkov, E.; Elizer, P.H.; Hagius, S.; O'Callaghan, D.; Let
Proc. Natl. Acad. Sci. U.S.A. 99, 443-448, 2002
A:Title: The genome sequence of the facultative intracellular pathogen Brucella melit
A:Reference number: AB3252; PMID:11756688

A:Accession: AC3582
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-494 <KUR>
A:Cross-references: GB:AE008918; PIDN:AAL53822.1; PID:g17984756; GSPDB:GN00191
A:Experimental source: strain 16M
A:Gene: BME10580
A:Map position: II

Query Match 12.6%; Score 402; DB 2; Length 494;
Best Local Similarity 26.4%; Pred. No. 1e-22;
Matches 142; Conservative 65; Mismatches 208; Indels 122; Gaps 17;

QY 56 ESPYNNLYRNALPIPVKOPKMITNPVTGKDIWYEIEIKPQOR-ITPTLRPATLVG 114
DB 7 KAP-----LPIPLVEP-----DASG-----IVRLVKQRSHSFAKSTVAAASG 46
QY 115 YDGMSPGPTFNVPRGTETVFRINNATVENSVHLGSPSRAPFDGMAEDVTPPEGKYD 174
DB 47 INGAVLGLPLVRLMSEESTLVSENMDEETILHMGLEVPSSHLDSGPHNVIAFGAKWEK 106
QY 175 PPNYASRLWYHDAFMKTAENAFEGQAGATYINDEADALGSPGGEFDIPLITAK 234
DB 107 VAVNGPASPFWPHPLHGHTRQAHMGIALIVBDGDAERGLBETGVDDLPVLDOR 166
QY 235 YYNADCTLRSTGE-----QDL-----MGDIYHNGQWPPLVNOVRKYRFRPLNAVS 284
DB 167 -----RVLEGDAVYAPDMDLHGRGDMVLVNGALAPARVPAAMVRLRLNGANA 218
QY 285 RAMLYLVRTSSPNRI-----PFOVIASDAGLQAPVQTSNLYLAVEREYIIIDTFNFA 340
DB 219 RNF-----HTRPADGRLLVIASDGGTISQPSVLEQTLIPGERIEVLVDFSN-- 266
QY 341 GQTLDRNVAETNDVDEDEYARTLEVMEFVYSSGIVEDNSQVPESTLDVPPPRKEGPA 400
DB 267 GEAVDLVTVGD--NGSGD-----GLHMRFTVDPALGEGVAKPVPVSLDGPAPDRLSVQ 319
QY 401 DKHFKFER-----SNGHYILNDVGFADVN----- 424
DB 330 RRSFFEDRMAENMKLNRQPSNPHASGDDMDHHEKSMAGMDHMGSRSAADAGPAL 379
QY 425 -----ERYLAKPELGTVEVWELENSSGSHPVHILVDFKILKRTG 466
DB 380 DALTSGVQALADKRFDMERIDVEAKLSWEIMEL--TSREAHAFPHIHGASFRLISNG 437
QY 467 GRGQVMPYESAGLKDVMWL--GRGETLTIEAHYQPTGAYVMHCHNLIHEDNDMAVF 522
DB 438 KK---PRAHQGWKMDTALIDGKAELIVHFDREARASHPFMFCHLHEHEDVGMAQF 491

RESULT 8

AB0523
Probable multicopper oxidase precursor [imported] - Salmonella enterica subsp. enteri
C:Species: Salmonella enterica subsp. enterica serovar Typhi
A:Note: this species has also been called Salmonella typhi
C:Date: 09-Nov-2001 #sequence_revision 09-Nov-2001 #text_change 09-Nov-2001
C:Accession: AF0523
R:Parkhill, J.; Dougan, G.; James, K.D.; Thomson, N.R.; Pickard, D.; Wain, J.; Church
th, T.; Connerton, P.; Cronin, A.; Davies, P.; Davies, R.M.; Dowd, L.; White, N.; Farr
S.; Moulé, S.; O'Gaora, P.
Nature 413, 848-852, 2001
A:Authors: Parry, C.; Quail, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens,
A:Title: Complete genome sequence of a multiple drug resistant Salmonella enterica se
A:Reference number: AB0502; PMID:11677608
A:Accession: AF0523
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-536 <PAR>

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: July 1, 2003, 10:33:51 ; Search time 24 Seconds

(without alignments)
1026.539 Million cell updates/sec

Title: US-10-080-233-2

Perfect score: 3189

Sequence: 1 MFKSMQLAASGLSLGVG.....AQEPYNRDELLEDGIEE 594

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

rchd: 112892 seqs, 41476328 residues

al number of hits satisfying chosen parameters: 112892

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Database : SWISSPROT 40.1*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1724.5	54.4	572	1	BILRO_MYRVE
2	713	22.4	513	1	COTR_BACSU
3	519	16.3	642	1	PHSA_STRAT
4	405.5	12.7	533	1	CUBO_YERPE
5	391	12.3	536	1	CUBO_SALTI
6	380	12.2	536	1	CUBO_SALTY
7	388.5	12.2	516	1	CUBO_ECOLI
8	385.5	12.1	516	1	CUBO_ECOS7
9	340.5	10.7	470	1	SUPL_ECOLI
10	323.5	10.1	470	1	SUPL_SALTY
11	241	7.6	311	1	SUPL_HAEIN
12	192.5	6.0	520	1	LAC1_TRAVI
13	192	6.0	609	1	COPA_PESM
14	188.5	5.9	520	1	LAC4_TRAVE
15	188.5	5.9	520	1	LAC4_TRAVE
16	185	5.8	527	1	LAC5_TRAVI
17	180	5.6	533	1	LAC2_PLEOS
18	180	5.6	621	1	LAC2_PODAN
19	179.5	5.6	605	1	PCOA_ECOLI
20	179.5	5.6	548	1	LAC1_PHLRA
21	179	5.6	520	1	LAC2_AGABI
22	177.5	5.6	619	1	LAC1_NEUCR
23	177	5.6	519	1	LAC2_TRAVI
24	176.5	5.5	519	1	LAC1_AGABI
25	176.5	5.5	620	1	LAC2_NEUCR
26	176	5.5	519	1	LAC1_CRYPA
27	174	5.5	520	1	LAC1_CORHI
28	172.5	5.4	552	1	ASO_CUCPM
29	171.5	5.4	552	1	ASO_CUCPM
30	169.5	5.3	519	1	LAC2_TRAVE
31	169.5	5.3	579	1	ASO_CUCMA
32	166.5	5.2	622	1	FET3_YEAST
33	163.5	5.1	624	1	FET3_CANAL

close

Adrian

Adrian

ALIGNMENTS

ID	BILRO_MYRVE	STANDARD	PRT	572 AA.
34	161.5	5.1	531	1
35	160.5	5.0	529	1
36	155.5	4.9	608	1
37	155.5	4.9	622	1
38	154	4.8	587	1
39	151.5	4.8	486	1
40	139.5	4.4	473	1
41	135.5	4.2	636	1
42	126.5	4.0	572	1
43	121	3.8	576	1
44	114	3.6	725	1
45	114	3.6	1115	1

RESULT 1

ID	BILRO_MYRVE	STANDARD	PRT	572 AA.
AC	012737			
DT	01-NOV-1997 (Rel. 35, Created)			
DT	01-NOV-1997 (Rel. 35, Last sequence update)			
DT	01-NOV-1997 (Rel. 35, Last annotation update)			
DE	Bilirubin oxidase precursor (EC 1.3.3.5).			
OS	Myrothecium verrucaria.			
OX	Eukaryota; Fungi; Ascomycota; mitosporic Ascomycota; Myrothecium.			
NCBI	taxid:5532;			
NCBI	[1]			
RC	SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.			
RC	SRRAIN-MT-1;			
RX	MEDLINE-93366794; PubMed-8360171;			
RA	Koike S., Ando K., Kajih H., Inoue T., Murao S., Takeuchi K., Samejima T.;			
RT	"Molecular cloning of the gene for bilirubin oxidase from Myrothecium verrucaria and its expression in yeast."			
RL	J. Biol. Chem. 268:18801-18809(1993).			
CC	FUNCTION: OXIDATION OF BILIRUBIN AND OTHER TETRAPYRROLES.			
CC	CATALYTIC ACTIVITY: Bilirubin + O(2) = biliverdin + H(2)O.			
CC	COFACTOR: THIS PROTEIN BELONGS TO THE MULTICOPPER OXIDASES WHICH CONTAIN THREE DISTINCT CU CENTERS KNOWN AS TYPE 1 OR BLUE, TYPE 2 OR NORMAL, AND TYPE 3 OR COUPLED BINUCLEAR. CONTAINS 2 BLUE COPPER ATOMS PER MOLECULE.			
CC	SIMILARITY: BELONGS TO THE FAMILY OF MULTICOPPER OXIDASES.			
CC	SIMILARITY: CONTAINS 2 PLASTOCYANIN-LIKE DOMAINS.			
CC	THIS SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/ or send an email to license@isb-sib.ch).			
CC	EMBL: D14081; BAA03166.1; -			
CC	EMBL: D12579; BAA02123.1; -			
DR	HSSP; P36649; 1KV7.			
DR	InterPro: IPR001117; Cu-oxidase.			
DR	Pfam: PF00394; Cu-oxidase; 1.			
KW	Signal; Copper; Metal-binding; Oxidoreductase; Glycoprotein; Repeat.			
FT	SIGNAL 1 19			
FT	PROPEP 20 38			
FT	CHAIN 39 572			
FT	DOMAIN 98 194			
FT	DOMAIN 404 526			
FT	METAL 132 132			
FT	METAL 134 134			
FT	METAL 172 172			
FT	METAL 174 174			
FT	METAL 436 436			
FT	METAL 439 439			
FT	METAL 441 441			
FT	METAL 494 494			
CC	BILIRUBIN OXIDASE.			
CC	PLASTOCYANIN-LIKE 1.			
CC	COPPER (TYPE 2) (BY SIMILARITY).			
CC	COPPER (TYPE 3) (BY SIMILARITY).			
CC	COPPER (TYPE 3) (BY SIMILARITY).			
CC	COPPER (TYPE 3) (BY SIMILARITY).			
CC	COPPER (TYPE 2) (BY SIMILARITY).			
CC	COPPER (TYPE 2) (BY SIMILARITY).			
CC	COPPER (TYPE 3) (BY SIMILARITY).			
CC	COPPER (TYPE 3) (BY SIMILARITY).			

FT METAL 495 495 COPPER (TYPE 1) (BY SIMILARITY).
 FT METAL 496 496 COPPER (TYPE 3) (BY SIMILARITY).
 FT METAL 500 500 COPPER (TYPE 1) (BY SIMILARITY).
 FT METAL 503 503 COPPER (TYPE 1) (BY SIMILARITY).
 FT CARBOHYD 510 510 N-LINKED (GLCNAC...) (POTENTIAL).
 FT CARBOHYD 520 520 N-LINKED (GLCNAC...) (POTENTIAL).
 SQ SEQUENCE 572 AA: 63947 MW: 5842D6413035E5EF CRC64;
 Query Match 54.1%; Score 1724.5; DB 1; Length 572;
 Best Local Similarity 60.3%; Pred. No. 8.6e-119;
 Matches 322; Conservative 75; Mismatches 128; Indels 9; Gaps 7;
 QY 57 SPYLLALRNALPPIPVVQPKMTITNPVTGCDIWEIEIKPQORITPTLPAVLGYD 116
 DB 43 SPQYP-METVLPPIPVVQPKMTITNPVTGCDIWEIEIKPQORITPTLPAVLGYD 101
 QY 117 GMSPGPTFNVPGSTFVVFRTINNAVENSVHLHSGSPAPFGMAEDTPECEYDYEP 176
 DB 102 GMSPGPTFNVPGSTFVVFRTINNAVENSVHLHSGSPAPFGMAEDTPECEYDYEP 161
 DB 177 NYQARLLMYHDHAFMKTAENAYFGAGAYIINDAEDALGPSYGEFDPILITAKY 236
 DB 162 NROSAKRLMYHDHAFMKTAENAYFGAGAYIINDAEDALGPSYGEFDPILITAKY 221
 QY 237 NADGTLRSTEGEDDODLMDVYHNGQPPFLNVQPKRFRFLNAVASRMLLYVTRSS 296
 DB 222 TANGSLVLTNGELNSFMDGVYHNGQPPFLNVQPKRFRFLNAVASRMLLYVTRSS 281
 QY 297 PNVRIPFOVIASDAGLLQAPVQTSNLYLAVERYYIIDFTFAGOTDLRNV-AETNDV 355
 DB 282 IDTRLRPFKVIASDAGLLQAPVQTSNLYLAVERYYIIDFTFAGOTDLRNV-AETNDV 341
 QY 356 GDEDEYARTLEVMRFVSSGVE-DNSQVPSLTLDVPP-PHKEGPADKHKFRERSNGY 413
 DB 342 GTDDYDVTMDVMRFVSSGVE-DNSQVPSLTLDVPP-PHKEGPADKHKFRERSNGY 399
 QY 414 LINDVGFADNVRNVLAKPELGEVWELENSGSGVHVIHNDKFLIKRGNG--QV 471
 DB 400 TINGVAFADNVRNVLAKPELGEVWELENSGSGVHVIHNDKFLIKRGNG--QV 459
 QY 472 MPYSAGLKVYVWLGRTETLIEAHYQWPTGAYMHCNLIHEDDMAVFNVTAMEBK 531
 DB 460 MPYSAGLKVYVWLGRTETLIEAHYQWPTGAYMHCNLIHEDDMAVFNVTAMEBK 518
 QY 532 YLODEDFEPPNPKRAVYNNRNDHARAGNSAESTIKARVQELAEQEPYNRLE 585
 DB 519 YNATVDFEPPNPKRAVYNNRNDHARAGNSAESTIKARVQELAEQEPYNRLE 572
 LT 2
 _BACSU STANDARD: PRT: 513 AA.
 AC POT788; 024818;
 DT 01-AUG-1988 (Rel. 08, Created)
 DT 30-MAY-2000 (Rel. 39, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Spore coat protein A.
 GN COTA OR FIG.
 OS Bacillus subtilis.
 OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
 OX NCBI_TaxID=1423;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-168;
 RX MEDLINE=97124186; PubMed=8969499;
 RA Borris R., Porwollik S., Schroeter R.;
 RT "The 52 degrees-55 degrees segment of the Bacillus subtilis
 chromosome: a region devoted to purine uptake and metabolism, and
 containing the genes cota, gap and gua and the pur gene cluster
 within a 34560 bp nucleotide sequence.";
 RL Microbiology 142:3027-3031(1996).
 RN [2]
 RP SEQUENCE FROM N.A.

RC STRAIN-168 / Marburg;
 RA MEDLINE=98116660; PubMed=9455482;
 RX Kasahara Y., Nakai S., Ogasawara N., Yata K., Sadate Y.;
 RT "Sequence analysis of the groEL-cota region of the Bacillus subtilis
 genome, containing the restriction/modification system genes.";
 RL DNA Res. 4:335-339(1997).
 RN [3]
 RP SEQUENCE OF 1-37 FROM N.A.
 RX MEDLINE=88011308; PubMed=2821284;
 RA Donovan W., Zheng L., Sandman K., Losick R.;
 RT "Genes encoding spore coat polypeptides from Bacillus subtilis.";
 RL J. Mol. Biol. 196:1-10(1987).
 RN [4]
 RP SEQUENCE OF 1-34 FROM N.A.
 RX MEDLINE=88286730; PubMed=3135411;
 RA Sandman K., Kroos L., Cutting S.M., Youngman P., Losick R.;
 RT "Identification of the promoter for a spore coat protein gene in
 Bacillus subtilis and studies on the regulation of its induction at a
 late stage of sporulation.";
 RL J. Mol. Biol. 200:461-473(1988).
 RN [5]
 RP SEQUENCE OF 1-10 FROM N.A.
 RC STRAIN-168;
 RA Wray L.V., Person A.E., Fisher S.H.;
 RL Submitted (JUL-1995) to the EMBL/GenBank/DBJ databases.
 CC -1- FUNCTION: INVOLVED IN BROWN PIGMENTATION DURING SPOROGENESIS.
 CC -1- SIMILARITY: TO S.ANTIBIOTICUS PHENOXAZINONE SYNTHASE (PNSA).
 CC -----
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 or send an email to license@sib-sib.ch).
 CC -----
 CC EMBL: U51115; AAB62305.1; -
 DR EMBL: AB007638; BAA22774.1; ALT_INIT.
 DR EMBL: Z99107; CAB12449.1; -
 DR EMBL: X05678; CAA29165.1; ALT_INIT.
 DR EMBL: X07512; CAA30392.1; -
 DR EMBL: U31756; AAC44642.1; -
 DR PIR: A27393; A27393.
 DR HSSP: P36649; IKV7.
 DR Subtilisin; B610490; cota.
 DR InterPro: IPR001117; Cu-oxidase.
 DR Pfam: PF00394; Cu-oxidase; 1.
 KW Sporulation; Complete proteome.
 FT CONFLICT 347 367 DESKPKYLASYPSYQHERIO -> TRAESTSTSPHILRYS
 FT FT MKDT (IN REF. 1).
 FT CONFLICT 414 420 PTRGTHP -> RHAHIL (IN REF. 1).
 FT FT GPAYVPPP -> VRCPPAA (IN REF. 1).
 SQ SEQUENCE 513 AA: 58499 MW: 836B83B458D75F87 CRC64;
 Query Match 22.4%; Score 713; DB 1; Length 513;
 Best Local Similarity 34.6%; Pred. No. 9e-45;
 Matches 183; Conservative 75; Mismatches 175; Indels 96; Gaps 18;
 QY 66 NALPPIPVVQPKMTITNPVTGCDIWEIEIKPQORITPTLPAVLGYDMSGP 121
 DB 8 DALPIPIPTLAKRVQO-----SKETIYEVMEECTHOLDLPPTRLMGVNGLPFG 57
 QY 122 PTFNVPGSTFVVFRTINNA-----EVENS-----VHLHSGSPAPFGD 159
 DB 58 PTIEVRKRNENYVWLMNNLPSTHFLPIDHTIHSDQHEPREVTVVHLHSGVTRPDDSDG 117
 QY 160 WAF-----DTFPEEY--KDYIPNTQASRLMYHDHAFMKTAENAYFGAGAYIIND 211
 DB 118 YPEAMFSKDEPOTPYKREYHYHPNOQRGAILMYHDHAFMKTAENAYFGAGAYIINDP 177
 QY 212 AEDALGPSYGEEDIPILITAKYNNADGTL--RSTEGEDQD-----MGDIYHV 259
 DB 178 KEKRLKLPSS--DEYDVPILITDRINEDGSLFSPADENPSLPNPSIYPAFCGETILV 235


```

OY 260 NCOPPELVNVOGRKRFREFRLNAAVSAMLLTYRRSSPNVRRIPFOYIASDAGLQAPVQT 313
Db 226 NCKWPVYLEVERKTRFRKYNASNTRTTSLSDNGD-----FIDIGSDGLPPRSVYL 289
OY 320 SNLYLAVAREYIIIDFTNFAQOTLDLRNVAET-NDVGDEDEYARFLEWRFPVSSGIVE 378
Db 290 NSFSLAPARERYDIIIDFTAYEESIIILANSACGGVNPETD-----ANIMQFRVTPPLAQ 345
OY 379 -DNSGVPESTLRDVPPEPKKEGPADKHFKERSNGHY----LINDGFADYNERVLAKPE 432
Db 346 KDESRRKPYXLASYPSVOHERIONITRLTKLAGTQDEYGRPVLLNNKRWHD---PYETPEK 402
OY 433 LGTFVWELENSGGSMSPVHTHLVDKFLTKR-----TGRGQVWPYES 476
Db 403 VGTTFWINSINTRG-TTHILHLVSLFRKLDLRPPDIARYQESGELSTYTGPAVPPPEK 461
OY 477 AGLKDVWMLGGETLTLEAHYQPMTGAYVMHCHNLIEDNDMAAFENVY 525
Db 462 -GMRKDTIQAHAGEVLRIAATFGPYSGRYVMCHILIEDHYDDMRPMDIT 509

RESULT 3
PHSA_STRAT PHSA_STRAT STANDARD; PRT; 642 AA.
AC Q53692;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE Phenoxazalone synthase (EC 1.-.-.) (Pfs)..
GN PHSA.
OS Streptomyces antibioticus.
OC Bacteria; Actinobacteria; Actinobacteria (Class); Actinobacteridae;
OC Actinomycetales; Streptomycetales; Streptomycetaceae; Streptomyces.
OX NCBI_Taxid=1890;
[1]
SEQUENCE FROM N.A., AND SEQUENCE OF 1-15.
RP STRAIN-IMU 3720;
RC MEDLINE=96011355; PubMed=7592317;
RA Hsieh C.-J., Jones G. H.;
RA "Nucleotide sequence, transcriptional analysis, and glucose
RT regulation of the phenoxazalone synthase gene (phsa) from
RL Streptomyces antibioticus.";
RL J. Bacteriol. 177:5740-5747(1995).
[2]
SUBUNITS.
RP MEDLINE=82066838; PubMed=7305384;
RX Choy H.A., Jones G. H.;
RX "Phenoxazalone synthase from Streptomyces antibioticus: purification
of the large and small enzyme forms.";
Arch. Biochem. Biophys. 211:55-65(1981).
-1- FUNCTION: CATALYZES THE LAST BUT TWO STEPS IN THE PUTATIVE
BIOSYNTHETIC PATHWAY OF ACTINOMYCIN.
-1- CATALYTIC ACTIVITY: 4,4-methyl-3-hydroxyanthraniloyl pentapeptide
+ 3 O(2) = 2 actinomycinic acid + 6 H(2)O.
-1- COFACTOR: THIS PROTEIN BELONGS TO THE MULTICOOPER OXIDASES WHICH
CONTAIN THREE DISTINCT CU CENTERS KNOWN AS TYPE 1 OR BLUE, TYPE
2 OR NORMAL, AND TYPE 3 OR COUPLED BINUCLEAR (BY SIMILARITY).
-1- SUBUNIT: HOMODIMER (SMALL FORM) OR HOMOHXAMER (LARGE FORM).
-1- SIMILARITY: BELONGS TO THE FAMILY OF MULTICOOPER OXIDASES.
-1- SIMILARITY: CONTAINS 2 PLASTOCYANIN-LIKE DOMAINS.
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EMBL: D04283; AAA86668.1; ALT_INTF.
DR HSSP; P36649; INV7.
OR InterPro: IPR001117; Cu-oxidase.

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Query Match	Best Local Similarity	Matches	Conservative	Score	DB	Length	DB 1	DB 2	DB 3	DB 4	DB 5	DB 6	DB 7	DB 8	DB 9	DB 10	DB 11	DB 12	DB 13	DB 14	DB 15	DB 16	DB 17	DB 18	DB 19	DB 20	DB 21	DB 22	DB 23	DB 24	DB 25	DB 26	DB 27	DB 28	DB 29	DB 30	DB 31	DB 32	DB 33	DB 34	DB 35	DB 36	DB 37	DB 38	DB 39	DB 40	DB 41	DB 42	DB 43	DB 44	DB 45	DB 46	DB 47	DB 48	DB 49	DB 50	DB 51	DB 52	DB 53	DB 54	DB 55	DB 56	DB 57	DB 58	DB 59	DB 60	DB 61	DB 62	DB 63	DB 64	DB 65	DB 66	DB 67	DB 68	DB 69	DB 70	DB 71	DB 72	DB 73	DB 74	DB 75	DB 76	DB 77	DB 78	DB 79	DB 80	DB 81	DB 82	DB 83	DB 84	DB 85	DB 86	DB 87	DB 88	DB 89	DB 90	DB 91	DB 92	DB 93	DB 94	DB 95	DB 96	DB 97	DB 98	DB 99	DB 100	DB 101	DB 102	DB 103	DB 104	DB 105	DB 106	DB 107	DB 108	DB 109	DB 110	DB 111	DB 112	DB 113	DB 114	DB 115	DB 116	DB 117	DB 118	DB 119	DB 120	DB 121	DB 122	DB 123	DB 124	DB 125	DB 126	DB 127	DB 128	DB 129	DB 130	DB 131	DB 132	DB 133	DB 134	DB 135	DB 136	DB 137	DB 138	DB 139	DB 140	DB 141	DB 142	DB 143	DB 144	DB 145	DB 146	DB 147	DB 148	DB 149	DB 150	DB 151	DB 152	DB 153	DB 154	DB 155	DB 156	DB 157	DB 158	DB 159	DB 160	DB 161	DB 162	DB 163	DB 164	DB 165	DB 166	DB 167	DB 168	DB 169	DB 170	DB 171	DB 172	DB 173	DB 174	DB 175	DB 176	DB 177	DB 178	DB 179	DB 180	DB 181	DB 182	DB 183	DB 184	DB 185	DB 186	DB 187	DB 188	DB 189	DB 190	DB 191	DB 192	DB 193	DB 194	DB 195	DB 196	DB 197	DB 198	DB 199	DB 200	DB 201	DB 202	DB 203	DB 204	DB 205	DB 206	DB 207	DB 208	DB 209	DB 210	DB 211	DB 212	DB 213	DB 214	DB 215	DB 216	DB 217	DB 218	DB 219	DB 220	DB 221	DB 222	DB 223	DB 224	DB 225	DB 226	DB 227	DB 228	DB 229	DB 230	DB 231	DB 232	DB 233	DB 234	DB 235	DB 236	DB 237	DB 238	DB 239	DB 240	DB 241	DB 242	DB 243	DB 244	DB 245	DB 246	DB 247	DB 248	DB 249	DB 250	DB 251	DB 252	DB 253	DB 254	DB 255	DB 256	DB 257	DB 258	DB 259	DB 260	DB 261	DB 262	DB 263	DB 264	DB 265	DB 266	DB 267	DB 268	DB 269	DB 270	DB 271	DB 272	DB 273	DB 274	DB 275	DB 276	DB 277	DB 278	DB 279	DB 280	DB 281	DB 282	DB 283	DB 284	DB 285	DB 286	DB 287	DB 288	DB 289	DB 290	DB 291	DB 292	DB 293	DB 294	DB 295	DB 296	DB 297	DB 298	DB 299	DB 300	DB 301	DB 302	DB 303	DB 304	DB 305	DB 306	DB 307	DB 308	DB 309	DB 310	DB 311	DB 312	DB 313	DB 314	DB 315	DB 316	DB 317	DB 318	DB 319	DB 320	DB 321	DB 322	DB 323	DB 324	DB 325	DB 326	DB 327	DB 328	DB 329	DB 330	DB 331	DB 332	DB 333	DB 334	DB 335	DB 336	DB 337	DB 338	DB 339	DB 340	DB 341	DB 342	DB 343	DB 344	DB 345	DB 346	DB 347	DB 348	DB 349	DB 350	DB 351	DB 352	DB 353	DB 354	DB 355	DB 356	DB 357	DB 358	DB 359	DB 360	DB 361	DB 362	DB 363	DB 364	DB 365	DB 366	DB 367	DB 368	DB 369	DB 370	DB 371	DB 372	DB 373	DB 374	DB 375	DB 376	DB 377	DB 378	DB 379	DB 380	DB 381	DB 382	DB 383	DB 384	DB 385	DB 386	DB 387	DB 388	DB 389	DB 390	DB 391	DB 392	DB 393	DB 394	DB 395	DB 396	DB 397	DB 398	DB 399	DB 400	DB 401	DB 402	DB 403	DB 404	DB 405	DB 406	DB 407	DB 408	DB 409	DB 410	DB 411	DB 412	DB 413	DB 414	DB 4
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ID	CUEO_YERPE	STANDARD:	PRT:	533 AA.
AC	CUEO_YERPE			
AD	08ZBK0:			
BT	15-JUN-2002 (Rel. 41, Created)			
DT	15-JUN-2002 (Rel. 41, Last sequence update)			
DR	15-JUN-2002 (Rel. 41, Last annotation update)			
DE	Blue copper oxidase cued precursor (Copper efflux oxidase).			
GN	CUEO OR YPO3409.			
OS	Versinia pests.			
OC	Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;			
OC	Versinia.			
OX	NCB1_TaxID=632;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	STRAIN-CO-92 / Bivovar Orientalis;			
RX	MEDLINE-21470413: PubMed-11586360;			
RA	Parshall J., Wren B.W., Thomson N.R., Tibball R.W., Holden M.T.G.,			
RA	Prentice M.B., Sebahlia M., James K.D., Churcher G., Mungall K.L.,			
RA	Baker S., Basham D., Bentley S.D., Brooks K., Cerdeno-Tarraga A.M.,			
RA	Chillingworth T., Cronin A., Davies R.M., Davis P., Dougan G.,			
RA	Feltwell T., Hamlin N., Holroyd S., Jagels K., Katlyshev A.V.,			
RA	Leather S., Moule S., Oyston P.C.F., Quail M., Ratlifford K.,			
RA	Simmmonds M., Skelton J., Stevens K., Whitehead S., Barrell B.G.;			
RF	"Genome sequence of Versinia pests, the causative agent of plague.";			
RL	Nature 413:523-527(2001).			
CC	-I- FUNCTION: Probably involved in periplasmic detoxification of			
CC	copper by oxidizing Cu(I) to Cu(II) and thus preventing its uptake			
CC	into the cytoplasm. Possesses phenoloxydase and ferrioxylase			
CC	activities and might be involved in the production of polyphenolic			
CC	compounds and the prevention of oxidative damage in the periplasm			
CC	(by similarity).			
CC	-I- COFACTOR: This protein belongs to the multicopper oxidases which			
CC	contain three distinct Cu centers known as type 1 or blue, type 2			
CC	or normal, and type 3 or coupled binuclear (by similarity).			
CC	-I- SUBUNIT: Monomer (Probable).			
CC	-I- SUBCELLULAR LOCATION: Periplasmic. It is exported via the Tat			
CC	pathway (By similarity).			
CC	-I- INDUCTION: By cuer, at increased levels of cytoplasmic cuprous			
CC	ions (Probable).			
CC	-I- DOMAIN: The methionine-rich domain could provide binding sites for			
CC	exogenous copper ions. This methionine-rich region is probably			
CC	important for copper tolerance in bacteria.			
CC	-I- SIMILARITY: BELONGS TO THE FAMILY OF MULTICOPPER OXIDASES.			
CC	-I- SIMILARITY: CONTAINS 3 PLASTOCOYANIN-LIKE DOMAINS.			
CC	-----			
CC	This SWISS-PROT entry is copyright. It is produced through a collaboration			
CC	between the Swiss Institute of Bioinformatics and the EMBL Outstation -			
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CC	use by non-profit institutions as long as its content is in no way			
CC	modified and this statement is not removed. Usage by and for commercial			
CC	entities requires a license agreement (see http://www.isb-sib.ch/announce/			
CC	or send an email to license@sib-sib.ch).			
CC	-----			
DR	EMBL; AJ14157; CAC92639.1; "			
DR	InterPro; IPR001117; Cu-oxidase.			
DR	InterPro; IPR002355; Multich_oxidse2.			
DR	Pfam; PF00394; Cu-oxidase; 1.			
DR	PROSITE; PS00080; MULTICOPPER_OXIDASE2; 1.			
KW	Oxidoreductase; Copper; Metal-binding; Periplasmic; Signal; Repeat;			
RM	Complete proteome.			
FT	SIGNAL	1..28		
FT	CHAIN	29..533	BY SIMILARITY.	
FT	DOMAIN	68..164	BLUE COPPER OXIDASE CUEO.	
FT	DOMAIN	165..425	PLASTOCOYANIN-LIKE 1.	
FT	DOMAIN	426..533	PLASTOCOYANIN-LIKE 2.	
FT	DOMAIN	356..415	PLASTOCOYANIN-LIKE 3.	
FT	METAL	102..102	MET-RICH.	
FT	METAL	104..104	COPPER (TYPE 2) (BY SIMILARITY).	
FT	METAL	142..142	COPPER (TYPE 3) (BY SIMILARITY).	
FT	METAL	144..144	COPPER (TYPE 3) (BY SIMILARITY).	
FT	METAL	458..458	COPPER (TYPE 1) (BY SIMILARITY).	
FT	METAL	461..461	COPPER (TYPE 2) (BY SIMILARITY).	
FT	METAL	463..463	COPPER (TYPE 3) (BY SIMILARITY).	

	FT	METAL	514	514	COPPER (TYPE 1) (BY SIMILARITY).
	FT	METAL	515	515	COPPER (TYPE 3) (BY SIMILARITY).
	FT	METAL	516	516	COPPER (TYPE 3) (BY SIMILARITY).
	FT	METAL	520	520	COPPER (TYPE 1) (BY SIMILARITY).
	FT	METAL	525	525	COPPER (TYPE 1) (BY SIMILARITY).
SQ	SEQUENCE	533 AA; 58328 MW; EDI570C9E9BIC135 CRC64;			
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Query Match 12.7%; Score 405.5; DB 1; Length 533:					
Best Local Similarity 27.1%; Pred. No. 3.2e-22;					
Matches 146; Conservative 57; Mismatches 217; Indels 119; Gaps 18					
OY		LPIPPVKKPK---MTITNPVTGKIDWYEIEIKPFQGRIRYPPLRATLV--GYDGSPGS	121		
		: : : : : : : : : : : :			
Db		LPPIPLLDPDANGKNLNIQTGSVWL-----PSTAIQTGWYGNLLG	76		
OY		122 PTFNVPGTETVFVEFINNAIVENSYLHSGPSRAFDGMADVPFEGEKDYFPNYSOA	181		
		: : : : : : : : : : : : : : :			
Db		PAIRLRGRKAVALTDITNLPRATTVMHGLEIPGEVDGPALLQPGAKRGTVFAEQPA	136		
OY		182 RLWTYHDIAFMFKTAENAFVGQAAGATIIDDEADAGLPSGSGEPDIPLITRAKYNNAGOT	241		
Db		137 ATCFWFHPHTHSKTGHQVAMGGVLILLDDSDSETPLRPKMGCVDDIPVILDDKLDRKHQ	196		
OY		242 LRTEGEDGOD-----WGDIVHNGCPMPFLNTVOPRKY-RPRFLNAAVSRAMLPLY	291		
Db		197 V-----DYOLDVMTAAVGFCDRLTLTGVIYP-QQLTRFGKVRLRLLNCAARSIALNL	249		
OY		292 VRTSSPNVRIFPVYIASDAGLIQAAPVOTSMLYLAVEERYEIITDFTNAGOTTDLRNAAE	351		
Db		250 -----SQRBMNYVASDGLLAEEVVYRELPILMGEFEVLVDTFRD--GQSILDVLTLPV	301		
OY		352 TNDVGDDEBEARTLEYMAEFVVS SGSEVEDNSGV-PSTLDVPPRRPKKEGRADKF-----	404		
Db		302 TOMGTALAPEPOPPLRVRIQPS---LATGSOVLPESLVVIDELADVTSVGDERFQMMDP	358		
OY		405 KFERSNCHYLII-----NDVGRFAD-----	422		
Db		359 KLDMIGMALVARYGMRKMMAGMNMNHGMGAMDHNCRDMSOGKKMGDHGMNCARPAN	418		
OY		423 ----VNERVLAKPE-----LGTEVWELEIENSSGSHPHVHLVDFLIKRTGGRGO	470		
Db		419 FSHNRIRINGKAFASMTPEAFDAKQGKEYEMWTISGEGDMAILHFPHVAGTOFRILTENG----	474		
OY		471 VMPE-SAGLDDVWL--GREPTLTIEAHYQPWGCAYMVHHOHNLHENDDMAVAVNYTA	526		
Db		475 KPPEHRHRGRMKDIVREGARSEILLRENYLAPASTPYMAHCHLLEDHEDTMGLGTVA	533		
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RESULT 5					
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ID_CUEO_SALT1					
AC		08JUN-2002 (Rel. 41, Created)			
DT		15-JUN-2002 (Rel. 41, Last sequence update)			
DT		15-JUN-2002 (Rel. 41, last annotation update)			
DE		Blue copper oxidase cueo precursor (copper efflux oxidase).			
GN		CUEO OR STY0190.			
OS		Salmonella typhi.			
OC		Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;			
CC		Salmonella.			
OX		NCB1_TaxID=601;			
RN		[1]			
RP		SEQUENCE FROM N.A.			
RC		STRAIN=Ct18;			
RX		MEDLINE=21534947; PubMed=11677608;			
RA		Parkhill J., Dougan G., James K.D., Thomson N.R., Pickard D., Main J.,			
RA		Churcher C., Mangall K.L., Bentley S.D., Holden M.T.G., Sebahin A.M.,			
RA		Baker S., Basham D., Brooks K., Chillingworth T., Connor P.,			
RA		Cronin A., Davis P., Davies R.M., Dowd L., White N., Farrar J.,			
RA		Feltwell T., Hamlin N., Haque A., Hien T.T., Holroyd S., Jagels K.,			
RA		Krogsh A., Larsen T.S., Leather S., Moule S., O'Gaora P., Parry C.,			
RA		Quail M., Rutherford B.K., Simmonds M., Skelton J., Stevens K.,			
RA		Whitehead S., Barrrell B.G.;			

CC -1- INDUCTION: By cuer, at increased levels of cytoplasmic cuprous
CC ions (probable).
CC -1- DOMAIN: The methionine-rich domain could provide binding sites for
CC exogenous copper ions. This methionine-rich region is probably
CC important for copper tolerance in bacteria.
CC -1- SIMILARITY: BELONGS TO THE FAMILY OF MULTICOPPER OXIDASES.
CC -1- SIMILARITY: CONTAINS 3 PLASTOCYANIN-LIKE DOMAINS.
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL: AY053397; AAL15149.1; -
DR EMBL: AE008702; AAL19132.1; -
CC StyGene: SG77777; cuco.
CC InterPro: IPR001117; Cu-oxidase.
CC Pfam: PF00394; Cu-oxidase; 1.
CC PROSITE: PS00080; MULTICOPPER OXIDASE2; 1.
DR Oxidoreductase; Copper; Metal-binding; Periplasmic; Signal; Repeat;
KM Complete proteome.
KM SIGNAL 1 28 BY SIMILARITY.
FT CHAIN 29 536 BLUE COPPER OXIDASE CUO.
FT DOMAIN 67 163 PLASTOCYANIN-LIKE 1.
FT DOMAIN 164 430 PLASTOCYANIN-LIKE 2.
FT DOMAIN 431 536 PLASTOCYANIN-LIKE 3.
FT DOMAIN 355 420 MET-RICH.
FT METAL 101 101 COPPER (TYPE 2) (BY SIMILARITY).
FT METAL 103 103 COPPER (TYPE 3) (BY SIMILARITY).
FT METAL 141 141 COPPER (TYPE 3) (BY SIMILARITY).
FT METAL 143 143 COPPER (TYPE 3) (BY SIMILARITY).
FT METAL 463 463 COPPER (TYPE 1) (BY SIMILARITY).
FT METAL 466 466 COPPER (TYPE 2) (BY SIMILARITY).
FT METAL 468 468 COPPER (TYPE 3) (BY SIMILARITY).
FT METAL 519 519 COPPER (TYPE 3) (BY SIMILARITY).
FT METAL 520 520 COPPER (TYPE 1) (BY SIMILARITY).
FT METAL 521 521 COPPER (TYPE 3) (BY SIMILARITY).
FT METAL 525 525 COPPER (TYPE 1) (BY SIMILARITY).
FT METAL 530 530 COPPER (TYPE 1) (BY SIMILARITY).
FT CONFLICT 322 323 LR -> F (IN REF. 1).
FT CONFLICT 334 334 L -> F (IN REF. 1).
SQ SEQUENCE 536 AA; 58625 MW; E4C04555AF621DF CRC64;
Query Match 12.2%; Score 390; DB 1; Length 536;
Best local similarity 25.8%; Pred. No. 4,4e-21;
Matches 140; Conservative 68; Mismatches 215; Indels 120; Gaps 18;
OY 65 RNALPPEVKKPKMTITNPVTGKDIWYIEIKPPQRIYPLIRATLVGVDGMSGPTF 124
DB 31 RALPPIPD-----LITADASNR-----MGLYKAGQSF--AGKNAITWGIVGNLGRAV 78
OY 125 NVPRGTEVVRFINNATVENSVHLHSGSPRAPFDGMAEDVTFPGYKDYPPNYOSARLL 184
DB 79 QLHGKSVTVDIHNOIADDTLLHMGLEIPGIVDGGPGIIRPAGSTRVTFPEQRAATC 138
OY 185 WYHDAEFKTEANAFVFGAGAVIINDEADNLGLPSGGEPIPLILRAKYINAGTILRS 244
DB 139 WIHPHKHGTGRQVAMGLAVLLEDDIRKLRLPKWGIIDVPIIIDKRSADGQI-- 196
OY 245 TEGEDQDL-----MGDVIHVGQWPEPLVNOVPRKRYRFRFLAAVSRALVLTFRS 295
DB 197 ----DYQIDMTAAVNGFGDILLTGATYTPQHSAPKGLRLKILNGCAARS-----LNTAA 248
OY 296 SPNVRIPOVIAASAGLLQAPVQSNLYLAVEREIIITFTNFAQGTLDLNNVAETNDV 355
DB 249 SDN--RPLVYIASDGLLAEPVKVTEPLPLMGEREVLVDISD--GKAFDLTVL--PVSGM 303
OY 356 G-----DEDEYARLEWRRVVSSTGIVEDNSOVFSTLDVDFPPHKAGPADKHKF--- 406

DB 304 GNAIAPFDKPHPMRIOPLR-ITASGT-----LPDITLTPMPLPSLEGLFVRNIKLSMD 356
OY 407 -----ERSNGHYLINDVGPAD----- 422
DB 357 PRLDMGQMMLKRTYGAQAMSGMDHSDNNAHMGSGHGEHDHGMDSGNHAGMGM 416
OY 423 -----VNERV--LAKP-----ELGTVWELENSSGWSHPVHILVDPKILK 463
DB 417 NHGKFDFFNANFINGQVFDNMKRPFAOKGRHERWVLSGVCDMLHPFHINGTOFRILS 476
OY 464 RTGGGQWMPYPSASGLKDYVWL--GRGETLITFAHYQFTGTAYMHCHLHEDNDMAV 521
DB 477 E---NGKAPAAHRTGMDTVREVGISEVLYKFDHDAKREHAYMAHCHLLEHEDGMMLG 533
OY 522 FNV 524
DB 534 FTV 536
RESULT 7
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ID CUEO_ECOLI STANDARD; PRI; 516 AA.
AC P36649; P75655; 01-JUN-1994 (Rel. 29, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Blue copper oxidase cuco precursor (Copper efflux oxidase).
GN CUEO OR B0123.
OS Escherichia coli.
OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
OX Escherichia.
OX NCBI_TaxID=562;
RP [1]
RP SEQUENCE FROM N.A.
RP STRAIN-K12 / W3110;
RC MEDLINE=94261430; PubMed=8202364;
RA Fujita N., Mori H., Yura T., Ishinuma A.;
RT "Systematic sequencing of the Escherichia coli genome: analysis of
RL the 2.4-4.1 min (110,917-193,643 bp) region."; Nucleic Acids Res. 22:1637-1639(1994).
RN [2]
RP SEQUENCE FROM N.A.
RP STRAIN-K12 / MG1655;
RC MEDLINE=97426617; PubMed=9278503;
RA Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland V.,
RA Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F.,
RA Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J.,
RA Mau B., Shao Y.;
RT "The complete genome sequence of Escherichia coli K-12."; Science 277:1453-1474(1997).
RN [3]
RP SEQUENCE OF 29-40.
RP STRAIN-K12 / EMG2;
RC MEDLINE=97443975; PubMed=9298646;
RA Link A.J., Rodison K., Church G.M.;
RT "Comparing the predicted and observed properties of proteins encoded
RL in the genome of Escherichia coli K-12."; electrophoresis 18:1259-1313(1997).
RN [4]
RP IDENTIFICATION BY MASS SPECTROMETRY.
RP MEDLINE=99420866; PubMed=10493123;
RA Fountoulakis M., Takacs M.-F., Berndt P., Langen H., Takacs B.;
RT "Enrichment of low abundance proteins of Escherichia coli by
RL hydroxyapatite chromatography."; electrophoresis 20:2181-2195(1999).
RN [5]
RP POSSIBLE FUNCTION IN COPPER HOMEOSTASIS.
RP MEDLINE=21125583; PubMed=11222619;
RA Grass G., Rensing C.;
RT "Genes involved in copper homeostasis in Escherichia coli."; J. Bacteriol. 183:2145-2147(2001).
RN [6]
RP POSSIBLE FUNCTION IN COPPER HOMEOSTASIS.

RC STRAIN-K12;
 RA MEDLINE-213391920; PubMed-11399769;
 RA Outten F.W., Huffman D.L., Hale J.A., O'Halloran T.V.;
 RT "The independent cue and cus systems confer copper tolerance during
 RT aerobic and anaerobic growth in *Escherichia coli*.";
 RL J. Biol. Chem. 276:30670-30677(2001).
 RN [7]
 RP CHARACTERIZATION.
 RC STRAIN-K12 / DH5-alpha;
 RX MEDLINE-20469457; PubMed-10915804;
 RA Outten F.W., Outten C.E., Hale J.A., O'Halloran T.V.;
 RT "Transcriptional activation of an *Escherichia coli* copper efflux
 RT regulon by the chromosomal merR homologue, *cueR*.";
 RL J. Biol. Chem. 275:31024-31029(2000).
 RN [8]
 RP CHARACTERIZATION.
 RC STRAIN-K12 / C600;
 RX MEDLINE-21359329; PubMed-11466290;
 RA Kim C., Lorenz W.W., Hoopes J.T., Dean J.F.D.;
 RT "Oxidation of phenolate siderophores by the multicopper oxidase
 RT encoded by the *Escherichia coli* *yacK* gene.";
 RL J. Bacteriol. 183:4866-4875(2001).
 RN [9]
 RP CHARACTERIZATION, AND MUTAGENESIS OF CYS-500 AND HIS-501.
 RC STRAIN-K12 / W3110;
 RX MEDLINE-21418784; PubMed-11527384;
 RA Grass G., Rensing C.;
 RT "CueO is a multi-copper oxidase that confers copper tolerance in
 RT *Escherichia coli*.";
 RL Biochem. Biophys. Res. Commun. 286:902-908(2001).
 RN [10]
 RP X-RAY CRYSTALLOGRAPHY (1.4 ANGSTROMS).
 RC STRAIN-K12 / W3110;
 RX MEDLINE-21874132; PubMed-11867755;
 RA Roberts S.A., Welch S.A., Grass G., Thakali K., Hazzard J.T.,
 RA Toller G., Rensing C., Montfort W.R.;
 RT "Crystal structure and electron transfer kinetics of CueO, a
 RT multicopper oxidase required for copper homeostasis in *Escherichia*
 RT *coli*.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:2766-2771(2002).
 RN [11]
 RP FUNCTION: Probably involved in periplasmic detoxification of
 RC copper by oxidizing Cu(I) to Cu(II) and thus preventing its uptake
 CC into the cytoplasm. Possesses phenoloxidase and ferroxidase
 CC activities and might be involved in the production of polyphenolic
 CC compounds and the prevention of oxidative damage in the periplasm.
 CC COFACTOR: This protein belongs to the multicopper oxidases which
 CC contain three distinct Cu centers known as type 1 or blue, type 2
 CC or normal, and type 3 or coupled binuclear.
 CC -1- SUBUNIT: Monomer (Probable).
 CC -1- SUBCELLULAR LOCATION: Periplasmic. It is exported via the Tat
 CC pathway.
 CC -1- INDUCTION: By cueR, at increased levels of cytoplasmic cuprous
 CC ions.
 CC -1- DOMAIN: The methionine-rich domain could provide binding sites for
 CC exogenous copper ions. This methionine-rich region is probably
 CC important for copper tolerance in bacteria.
 CC -1- MISCELLANEOUS: This protein is sensitive to oxygen deprivation. It
 CC probably plays a significant role in copper efflux under aerobic
 CC conditions.
 CC -1- SIMILARITY: BELONGS TO THE FAMILY OF MULTICOPPER OXIDASES.
 CC -1- SIMILARITY: CONTAINS 3 PLASTOCYANIN-LIKE DOMAINS.
 CC -1- CAUTION: REF.1 SEQUENCE DIFFERS FROM THAT SHOWN DUE TO A
 CC FRAMESHIFT IN POSITION 464.
 CC
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 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
 CC or send an email to license@sib-sb.ch).
 CC
 CC EMBL, D26562; BAA05579.1; ALT_FRAME.

DR EMBL: AE000121; AAC73234.1;
 DR PIR: S45200; S45200.
 DR PDB: 1KV7; 06-FEB-02.
 DR Ecogene: EG12318; cueO.
 DR InterPro: IPR001117; Cu-oxidase.
 DR InterPro: IPR002355; MultiCu_oxidase2.
 DR Pfam: PF00394; Cu-oxidase; 1.
 DR PROSITE: PS00080; MULTICOPPER_OXIDASE2; 1.
 KW Oxidoreductase; Copper; Metal-binding; Periplasmic; Signal; Repeat;
 FT 3D-structure; Complete proteome.
 FT SIGNAL 1 28
 FT CHAIN 29 516 BLUE COPPER OXIDASE CUEO.
 FT DOMAIN 67 163 PLASTOCYANIN-LIKE 1.
 FT DOMAIN 164 410 PLASTOCYANIN-LIKE 2.
 FT DOMAIN 411 516 PLASTOCYANIN-LIKE 3.
 FT DOMAIN 355 400 MET-RICH.
 FT METAL 101 101 COPPER (TYPE 2).
 FT METAL 103 103 COPPER (TYPE 3).
 FT METAL 141 141 COPPER (TYPE 3).
 FT METAL 143 143 COPPER (TYPE 3).
 FT METAL 443 443 COPPER (TYPE 1).
 FT METAL 443 443 COPPER (TYPE 1).
 FT METAL 446 446 COPPER (TYPE 2).
 FT METAL 448 448 COPPER (TYPE 3).
 FT METAL 499 499 COPPER (TYPE 3).
 FT METAL 500 500 COPPER (TYPE 1).
 FT METAL 501 501 COPPER (TYPE 3).
 FT METAL 505 505 COPPER (TYPE 1).
 FT METAL 510 510 COPPER (TYPE 1).
 FT METAL 510 510 COPPER (TYPE 1).
 FT MOTIF 500 501 CH-SR: RESIDUAL ACTIVITY AND LOSS OF
 FT RESISTANCE TO COPPER.
 SQ SEQUENCE 516 AA; 56556 MW; 37D96B1C331CF30B CRC64;
 Query Match 12.28; Score 388.5; DB 1; Length 516;
 Best Local Similarity 26.18; Pred. No. 5.3e-20;
 Matches 142; Conservative 65; Mismatches 208; Indels 129; Gaps 19;
 66 NALPI-----PVRQPKMIIITPVGKIDWIYEIEIKPQORITPL----- 107
 17 SALPIMSRATFAAEERPLTPIPLDLTTDA-----RRRIQLTLTGAGSTFG 60
 108 -RPATLVGIDGMSPTGFENVRKGTETVVRFINNATVENSVAHLGSPSRAPFDGMAEDVTF 166
 61 GKATATGWYGNLGLPAVKLQKGAIVVDIYNLTERTLHMGLLEVPGEVGGPGGIIP 120
 167 PGEYKDYFFNYSARILWHDHAFKMTAFNAPFGAGATYINDAEDALGTSVGEED 226
 121 PGGKRSYTLNVDPAPATCMFPHQHGKGVAMGLAGLVIEDDELTKMLPRQWGIID 180
 227 IPIILTAKYNNADGTLRSTGEEDQD-----MGDVIVNGQPPFLNVOPRKY-RF 276
 181 VPIVYDQDKRSADGQI-----DYQDVMFAAGVCRDILLTGATYIP-QHAAPRGKRL 233
 277 RFLNAAVSRAMLLYVTRTSSPNVRIPROVIASAGLLQADVQTSNYLAVEREITIDF 336
 234 RLINGCNARS-----LNFATSDN--RPLVYIASDGLLEPVKVSLEPLVGEFEVLEVEV 287
 337 TN---FAGQTLDRNVAETFDVDEDEYATILVMRFVSSGVEDNSQVPSLRYVRF 393
 288 NDKKRPDLVTLVPSQMGMA--IAPFDKPHVMRIQPIAISA-----SGALPDTLSSLPAL 340
 394 PHEKGRPA-----DKH----- 403
 341 PSLGGLTVKRLQSLMDPMLDMGMOMLMEKYGQAMAGMDHSGMGMHGMNHNHNG 400
 404 -FFEESNGHYLLINDVGFADYNERVYLAKEPLGLVEYWELENSGGSHPVHNLVDFKLL 462
 401 KFDFFHAN--KINGQAF-DMNKPMPAAK-GQYEWVVISGVDDMLHPFHINGTOFRILL 455
 463 KRTGGRGOVWPYESAGIKDYVVL--GRGETLTLEAHYQPTGATGMHCHNLTHEDDDMA 520
 456 SE---NGKPPAAHRAQMKDTIVKGVNSEVLYKFNDAPEHRAHYMAHCHLLEDYGMML 512
 521 VENV 524

Db 513 GFTV 516

RESULT 8
CUEO_ECO57 STANDARD; PRT; 516 AA.
AC Q8X947;
DT 15-JUN-2002 (Rel. 41, Created)
DT 15-JUN-2002 (Rel. 41, Last sequence update)
DE 15-JUN-2002 (Rel. 41, Last annotation update)
DE Blue copper oxidase cueo precursor (copper efflux oxidase).
GN CUEO OR 20133 OR ECS0127.
OS Escherichia coli O157:H7.
OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae; Escherichia.
OX NCBI_TaxID=83334;
RN [1]
RM SEQUENCE FROM N.A.
RA STRAIN=O157:H7 / EDL933 / ATCC 700927;
RA MEDLINE=21074935; PubMed=11206551;
RA Perna N.F., Plunkett G. III, Burland V., Mau B., Glasner J.D., Rose D.J., Mayhew G.F., Evans P.S., Gregor J., Kirkpatrick H.A., Goddard G., Hackett J., Klink S., Boutin A., Shao Y., Miller L., Grobbeck E.J., Davis N.W., Lim A., Dimalanta E.T., Potamocis K., Apodaca J., Anantharaman T.S., Lin J., Yen G., Schwartz D.C., Welch R.A., Blattner F.R.;
RA "Genome sequence of enterohaemorrhagic Escherichia coli O157:H7";
RA Nature 409:529-533(2001).
RL [2]
RN SEQUENCE FROM N.A.
RP STRAIN=O157:H7 / RMD 0509952;
RX MEDLINE=21156231; PubMed=11258796;
RA Hayashi T., Makino K., Ohnishi M., Kurokawa K., Ishii K., Yokoyama K., Han C.-G., Ohtsubo E., Nakayama K., Murata T., Tanaka M., Tobe T., Iida T., Takami H., Honda T., Sasakawa C., Ogasawara N., Yasunaga T., Kudara S., Shiba T., Hattori M., Shinagawa H.;
RA "Complete genome sequence of enterohaemorrhagic Escherichia coli O157:H7 and genomic comparison with a laboratory strain K-12";
RA DNA Res. 8:11-22(2001).
RL
CC -1- FUNCTION: Probably involved in periplasmic detoxification of copper by oxidizing Cu(I) to Cu(II) and thus preventing its uptake into the cytoplasm. Possesses phenoloxidase and ferroxidase activities and might be involved in the production of polyphenolic compounds and the prevention of oxidative damage in the periplasm (By similarity).
CC -1- COFACTOR: This protein belongs to the multicopper oxidases which contain three distinct Cu centers known as type 1 or blue, type 2 or normal, and type 3 or coupled binuclear (By similarity).
CC -1- SUBUNIT: Monomer (Probable).
CC -1- SUBCELLULAR LOCATION: Periplasmic. It is exported via the Tat pathway (By similarity).
CC -1- INDUCTION: By cueR, at increased levels of cytoplasmic cuprous ions (Probable).
CC -1- DOMAIN: The methionine-rich domain could provide binding sites for exogenous copper ions. This methionine-rich region is probably important for copper tolerance in bacteria.
CC -1- SIMILARITY: BELONGS TO THE FAMILY OF MULTICOPPER OXIDASES.
CC -1- SIMILARITY: CONTAINS 3 PLASTOCYANIN-LIKE DOMAINS.
CC
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CC
CC EMBL: AE005188; BAG54427.1; -
CC EMBL: AP002550; BAB33550.1; -
CC InterPro: IPR001117; Cu-oxidase.
CC InterPro: IPR002355; Multicup_oxidase2.
CC Pfam: PF00394; Cu-oxidase; 1.

DR PROSITE: PS00080; MULTICOPPER_OXIDASE2; 1.
KW Oxidoreductase; Copper; Metal-binding; Periplasmic; Signal; Repeat;
KW Complete proteome.
FT SIGNAL 1 28 BY SIMILARITY.
FT CHAIN 29 516 BLUE COPPER OXIDASE CUEO.
FT DOMAIN 67 163 PLASTOCYANIN-LIKE 1.
FT DOMAIN 164 410 PLASTOCYANIN-LIKE 2.
FT DOMAIN 411 516 PLASTOCYANIN-LIKE 3.
FT DOMAIN 355 400 MET-RICH.
FT METAL 101 101 COPPER (TYPE 2) (BY SIMILARITY).
FT METAL 103 103 COPPER (TYPE 3) (BY SIMILARITY).
FT METAL 141 141 COPPER (TYPE 3) (BY SIMILARITY).
FT METAL 143 143 COPPER (TYPE 3) (BY SIMILARITY).
FT METAL 443 443 COPPER (TYPE 1) (BY SIMILARITY).
FT METAL 446 446 COPPER (TYPE 2) (BY SIMILARITY).
FT METAL 448 448 COPPER (TYPE 3) (BY SIMILARITY).
FT METAL 499 499 COPPER (TYPE 3) (BY SIMILARITY).
FT METAL 500 500 COPPER (TYPE 1) (BY SIMILARITY).
FT METAL 501 501 COPPER (TYPE 3) (BY SIMILARITY).
FT METAL 505 505 COPPER (TYPE 1) (BY SIMILARITY).
FT METAL 510 510 COPPER (TYPE 1) (BY SIMILARITY).
SQ SEQUENCE 516 AA; 56702 MW; 7AD387C79780386 CRC64;
Query Match 12.1%; Score 385.5; DB 1; Length 516;
Best local similarity 25.9%; Pred. No. 8.8e-21;
Matches 141; Conservative 66; Mismatches 208; Indels 129; Gaps 19;
OY 66 NALPI-----PPYKPKMTITNVTKDVIYEIEIKPPQQRITPL----- 107
DB 17 SALPLSVAFVAFERPLIPDLTLTDA-----RNRIQLTIGAGQSTFG 60
OY 108 -RPATLVGDSMSPTFENVPRGTETVRFINNATVENSVALHGPSRAPFGWAEDVTF 166
DB 61 EKTATWYQYNNILGPAKLRKAVYDIYNOLTEETLTHMGLVNGEVDGGRPGIIP 120
OY 167 PGEYKDYFFPNYQARLLMYHDHAFMKTAENAYFGQAGAYIINDAEDALGPGYGEFD 226
DB 121 PGKRSVTLVNDQPAATCFWPHQHGKTRGVAMGLAVIETDELLKMLPKWGIID 180
OY 227 IPLLTLKYNVADGTLRSTBEEDDL-----WGVHVNQMPFLVQPRKY-RE 276
DB 181 VPIVVDKFFSADQI-----DYQLDMTAAGVFGDTLLTNATLP-QHAAPRGWRL 233
OY 277 RFLNAVSRAMLTLVRTSSPNVRLIPQVIAADGLQAPQTSNLYLAVEREIIIDF 336
DB 234 RLNGCARNR-----LNRATSDN--RPLVIAISDGLLPEPKVVELPLMKEERELVEV 287
OY 337 TN---FAGQTLDRNVAETNDVGDDEYARTLEVRRVYSSGTVEDNSQVSTLDVPEP 393
DB 288 NDNKPFDLVTLPLVSQMGWA--IAPFDKPPHMPRIOTPAISA-----SGALPDLTSSPAL 340
OY 394 PKRGPA-----DKH----- 403
DB 341 PSLGLTVRKQLSMDPMLDMGMOMLEKQGDQAVGMDSQMGHMGNNHMHNG 400
OY 404 -FKFERSNGHYLINDVGFADVNERVLAKPELGTVEVELESSGSGSHVPIHLVDKIL 462
DB 401 KFDHNNH---KINGQAF-DNNKPMFAAK-GQYERWIVISVGDMMLPFRIHGTQRIIL 455
OY 463 KRTGRCQVMPYESAGLKVYVL--GGETITLFAHYQPTGAYMMCHNLIHEDDMA 520
DB 456 SE---NCKPRAHRAQWMDVFKVGNSEVLYVKNFHDAKPERAYAMACHLLEHBDTGML 512
OY 521 VENV 524
DB 513 GFTV 516

RESULT 9
SUFL_ECOLI STANDARD; PRT; 470 AA.
ID SUFL_ECOLI
AC P26648;
DT 01-AUG-1992 (Rel. 23, Created)

DT 01-NOV-1995 (Rel. 32, Last sequence update)
 DE 16-OCT-2001 (Rel. 40, Last annotation update)
 DR Protein sufi precursor.
 OS SUFI OR B3017.
 OC Escherichia coli.
 OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
 OC Escherichia.
 NCBI_Taxid=562;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-K12 / MG1655;
 RX BLATNER F.R., PLUNKETT G. III, BLOCH C.A., PERNA N.T., BURLAND V.,
 RILEY M., COLLADO-VIDES J., GLASNER J.D., RODE C.K., MAYHEW G.F.,
 GREGOR J., DAVIS N.W., KIRKPATRICK H.A., GOEDEN M.A., ROSE D.J.,
 MAU B., SHAO Y.,
 RL "The complete genome sequence of Escherichia coli K-12.";
 Science 277:1453-1474(1997).
 [2]
 RN [2]
 RP SEQUENCE OF 1-89 FROM N.A.
 RC MEDLINE=92212294; PubMed=1557036;
 RX COLEMAN J.;
 RL "Characterization of the Escherichia coli gene for
 1-acyl-sn-glycerol-3-phosphate acyltransferase (Plsc).";
 Mol. Gen. Genet. 232:295-303(1992).
 [3]
 RN [3]
 RP SEQUENCE OF 28-39.
 RC STRAIN-K12 / EMG2;
 RX MEDLINE=97443975; PubMed=9298646;
 RA LINK A.J., ROBISON K., CHURCH G.M.;
 RL "Comparing the predicted and observed properties of proteins encoded
 in the genome of Escherichia coli K-12.";
 Electrophoresis 18:1259-1313(1997).
 CC -1- FUNCTION: INVOLVED IN CELL DIVISION, SUPPRESSES A FIRST MUTATION.
 CC -1- SUBCELLULAR LOCATION: Periplasmic.
 CC -1- SIMILARITY: CONTAINS 1 PLASTOCYANIN-LIKE DOMAIN.
 CC
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 CC
 DR EMBL: U28377; AAA69185.1;
 DR EMBL: AE000384; AAC76053.1;
 DR EMBL: M63491; AAA24398.1;
 PIR: S20461; S20461.
 HSSP: P36649; 1KV7.
 EC: Ecocore: EG11376; sufi.
 InterPro: IPR001117; Cu-oxidase.
 DR Pfam: PF00394; Cu-oxidase; 1.
 KW Periplasmic; Signal; Complete proteome.
 FT SIGNAL 1 27
 FT CHAIN 28 470 PROTEIN SUFI.
 FT DOMAIN 68 164 PLASTOCYANIN-LIKE.
 SO SEQUENCE 470 AA; 51858 MW; C6435ACB146688 CRC64;
 Query Match 10.7%; Score 340.5; DB 1; Length 470;
 Best Local Similarity 26.9%; Pred. No. 1.5e-17;
 Matches 139; Conservative 62; Mismatches 176; Indels 139; Gaps 20;
 QY 20 GIPMDGSHIEAVDEVKTEVFADSLAAGDDWESPYNLLIRALDIPYKQPKMT 79
 DB 13 GAGCAGAVPLK-----SAAG-----QDFVPLLESR- 43
 QY 80 ITNPVTKDIWYEIEIKPROGRIYPLRP---ATLVGYGMSGPFPNPRGRTYVRF 136
 DB 44 -RGQPLFM-----TVQRAHMSFTGTASVWGINGRILGPIIRYWKGDVXLYI 91
 QY 137 INNATYENSV-----HLHGSPSR--APFDGMADVTVPGEYKDYFPNYSARILW 185

DB 92 SNRLTENVSMTVAGIQAQVPCGLMGSPARHMSPNADMD-----VLPIRONAATLW 140
 QY 186 YHDAEFKTKTAEAFAGAGAYIINDEADALGPSGGERDIPILITAKYINADGTRST 245
 DB 141 YHANTPRTAQOYVYNGLAGMVLVEVSKSLPIPNHGVDFPVIIDKRLDNFGPEYN 200
 QY 246 EGEDQDLMGVIVHNGPMPFELNVAQPKRYRFRFRAVRAVAMLLYLVRSSPNRIPFOV 305
 DB 201 EPGSGGVGDTLVLVNGVQSPFVEVSRGVRLRLNANSNRKRYQOM-----NDGRPLHV 254
 QY 306 IASDAGLLQAPVQTSNLYLAVEREITIDFTNAGOTDLRLNVAETNDVGE-----DE 360
 DB 255 ISGQGLPAPVSVKQSLALPGERREILVDMN-----GDEVSIKGE 297
 QY 361 YARLEVMRRVSSGTYEDNSQVSTL-----RDVPPPKKEPAD 401
 DB 298 AASTVDRIK-----GFEPSSTLSTVLRLPTGLPLVYDLSLPMLLPLEIMAGSPI- 351
 QY 402 KHEFKERSNGHYLLINDGFA---DNERVYLAKPELGTVEVMELENSSGMSHPVHLV 457
 DB 352 -----KSRLISLGDDEGINGQMLDVN-RIDVTAQGGTWERMYRADE---PQAFHIEGV 401
 QY 458 DFKILKRTGRGVMPY-ESAGLKDVWL-GRGETL 491
 DB 402 MFLIRNVNG-----AMPPEDRGMKDTVMVQGVETL 433
 RESULT 10
 SUFI_SALTY STANDARD; PRT; 470 AA.
 AC P40799;
 DT 01-FEB-1995 (Rel. 31, Created)
 DT 15-JUN-2002 (Rel. 41, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Protein sufi precursor.
 GN SUFI OR STM3172 OR STY3349.
 OS Salmonella typhimurium, and
 OS Salmonella typhi.
 OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
 OC Salmonella.
 NCBI_Taxid=602, 601;
 OX [1]
 RN [1]
 RP SEQUENCE FROM N.A.
 RC SPECIES-S.typhimurium; STRAIN-LT2;
 RA Cong J., Schmid M.B.;
 RL Submitted (APR-1994) to the EMBL/GenBank/DBJ databases.
 [2]
 RN [2]
 RP SEQUENCE FROM N.A.
 RC SPECIES-S.typhimurium; STRAIN-LT2 / SGSC1412 / ATCC 700720;
 RX MEDLINE=21534948; PubMed=11677609;
 RA McCelland M., Sanderson K.E., Spiehl J., Clifton S.W., Latreille P.,
 Courtney L., Potwillok S., Ali J., Dante M., Du F., Hou S., Layman D.,
 Leonard S., Nguyen C., Scott K., Holmes A., Grewal N., Mulvaney E.,
 Ryan E., Sun H., Flores L., Miller W., Stoneking T., Nhan M.,
 Waterston R., Wilson R.K.;
 RL "Complete genome sequence of Salmonella enterica serovar Typhimurium
 LT2.";
 Nature 413:852-856(2001).
 [3]
 RN [3]
 RP SEQUENCE FROM N.A.
 RC SPECIES-S.typhi; STRAIN-CF18;
 RX MEDLINE=21534947; PubMed=11677608;
 RA Parkhill J., Dougan G., James K.D., Thomson N.R., Pickard D., Wain J.,
 Baker S., Basham D., Brooks K., Chillingworth T., Connor P.,
 Cronin A., Davis P., Davies R.M., Dowd L., White N., Farrar J.,
 Felwell T., Hamlin N., Haque A., Hien T.F., Holroyd S., Jagels K.,
 Krogue A., Larsen T.S., Leather S., Moule S., O'Goira P., Parry C.,
 Quail M., Rutherford K., Simmonds M., Skelton J., Stevens K.,
 Whitehead S., Barrett B.G.;
 RL "Complete genome sequence of a multiple drug resistant Salmonella
 enterica serovar Typhi CF18.";
 Nature 413:848-852(2001).

Search completed: July 1, 2003, 10:39:24
Job time : 27 secs

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CC -1- FUNCTION: INVOLVED IN CELL DIVISION, SUPPRESSES A FTSI MUTATION
CC (BY SIMILARITY).
CC -1- SUBCELLULAR LOCATION: Periplasmic (By similarity).
CC -1- SIMILARITY: CONTAINS 1 PLASTOCYANIN-LIKE DOMAIN.
CC -1- CAUTION: Ref.1 sequence differs from that shown due to a
CC frameshift in position 413.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
CC DR EMBL: U09309; AAA56679.1; ALT_FRAME.
CC DR EMBL: AE008845; AAL22046.1; -.
CC DR EMBL: AL627277; CAD03004.1; -.
CC DR HSSP: P36649; IKV7.
CC StyGene; SG10522; sufl.
CC InterPro; IPR001117; Cu-oxidase.
CC Pfam; PF00394; Cu-oxidase; 1.
CC Periplasmic; Signal; Complete proteome.
CC FT SIGNAL 1 27 BY SIMILARITY.
CC FT CHAIN 28 470 PROTEIN SUFI.
CC FT DOMAIN 68 164 PLASTOCYANIN-LIKE.
CC SEQUENCE 470 AA; 51858 MW; 61B84D4D2B025FB CRC64;

Query Match 10.1%; Score 323.5; DB 1; Length 470;
Best Local Similarity 25.8%; Pred. No. 2.7e-16;
Matches 142; Conservative 58; Mismatches 190; Indels 161; Gaps 21;

QY 1 MLFKSMQLAASGLISGLVLPMDGSHPIEAVDEPVEKTEVPADSLAAGDDDMESPPY 60
DB 1 MSFSRQFLQAS-----GIALCAGATPLRA-----NAAGQ----- 30
QY 61 NLVYRNALPIPPVAKOPKMITNPVTGKDIWYEIEIKPPQQRITPLR-----PA 110
DB 31 ----QQLPVPPLLESRR-----GQPLFMTLQRAHWSFTQGTTRA 65
QY 111 TLVGYDGMSPGTFVPRGTETVVFINNATYENSV-----HLHGSPSR--APFDG 159
DB 66 FWMGVNGRRYLGPTLRWKGDDVKLYSNRLAENVSMYVAGLIVPGPLMGGPARMSPNAD 125
QY 160 WAEDVTFPEYKDYFPNYQSAKRLMYHDHAFMKTAENAYFGQAGAYIINDAEADALGP 219
DB 126 WAP-----VLPIRQSAATLWYHANTPNRTAQYVNGLAGMMLVEDDISKTLPIP 174
QY 220 SGYGEFDIPLILTAKYNAADGTLNSTEGEDODLMDGVTHVNGQMPWFLNVQPKYRFRFL 279
DB 175 NHGYVDDEPVIIDKRLNFGTPEXSEPGSGFGVDTLVNGAQSPYVEVSRGWRLRL 234
QY 280 NAAVSRAVLVLRTPSPNVRIPFQYIASDAGLLQAPQTSNLVLAVEREIIIDTFNF 339
DB 235 NANSRRYQLOMSDGRA-----LHAVISGDQGLPAPVSVKOLSLAPGERREIIVDMTN- 287
QY 340 AGQTLDLRNVAETNDVDE-----DEVARTLEVRFVSVSGTVEDNSQVPSL----- 387
DB 288 -----GDEVSTTCGEAASYDRIR-----GFEPPSSILVSTLVLTLPRT 326
QY 388 -----RDVYPPPHKEGPAKHFKEFSNGHYLLINDVGA---DYNERVLAKP 431
DB 327 GLPLVLTNLPMLRLPTEIMSGAPV-----RSRDISLGDDPGINGQLMDVN-RIDITA 378
QY 432 ELGTYEWELENSGCGMHPVHIHLVDFKILKRTGSGQVMPY-ESAGIKDYVMGLRGRT 490
DB 379 QQGTWERTVTR---ADMPOSFHEIGSVSLIRVNG---AMFEPEDRGMKDTVMVD-GQV 430
QY 491 LTIENHYOP-W 500
DB 431 ELLVYYGQPSW 441
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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: July 1, 2003, 10:36:21 ; Search time 86 Seconds
(without alignments)
1423.163 Million cell updates/sec

Title: US-10-080-233-2

Sequence: 1 MFKSWQLAASGLSLGVLG.....AEQEPYRLDELIDEGIEE 594

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Number of hits satisfying chosen parameters: 671580

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database :

- 1: SPREMBL_21.*
- 2: sp_archaea.*
- 3: sp_bacteria.*
- 4: sp_fungi.*
- 5: sp_human.*
- 6: sp_invertebrate.*
- 7: sp_mammal.*
- 8: sp_mhc.*
- 9: sp_organelle.*
- 10: sp_plant.*
- 11: sp_protist.*
- 12: sp_virus.*
- 13: sp_vertebrate.*
- 14: sp_unclassified.*
- 15: sp_virus.*
- 16: sp_bacteriophage.*
- 17: sp_archaeal.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1705	53.5	602	09P8C3	09P8C3 acromonium
2	612.5	19.2	475	093M03	093M03 streptomyc
3	513	16.1	431	08RMC6	08RMC6 streptomyc
4	497.5	15.6	582	09AMU4	09AMU4 oryza sativ
5	480	15.1	568	023123	023123 arabidopsis
6	465	14.6	581	0949X9	0949X9 arabidopsis
7	464	14.6	637	09PTS3	09PTS3 oryza sativ
8	459	14.4	581	08W4N2	08W4N2 arabidopsis
9	450	14.1	591	09C9A4	09C9A4 arabidopsis
10	439.5	13.8	527	067206	067206 aquifex aeo
11	432	13.5	614	09PTS5	09PTS5 oryza sativ
12	430.5	13.3	588	09PTS6	09PTS6 oryza sativ
13	423.5	12.6	502	09BFW8	09BFW8 rhizobium
14	402	11.8	494	08ICF0	08ICF0 brucella me
15	375.5	11.8	515	09CJ06	09CJ06 pasteurella
16	375	11.8	477	08XW8	08XW8 pyrobaculum

17	335.5	10.5	470	08XBS6	08XBS6 escherichia
18	315.5	9.9	513	09PME8	09PME8 campylobact
19	310	9.7	468	09CEP1	09CEP1 pasteurella
20	303	9.5	474	08Z141	08Z141 yersinia pe
21	284	8.9	1662	2 P71431	P71431 leptothrix
22	236.5	7.4	460	2 09X3V2	09X3V2 pseudomonas
23	236	7.4	589	3 09C497	09C497 glomerella
24	235.5	7.4	717	16 08XPV6	08XPV6 raietonia s
25	231.5	7.3	570	16 09A9L6	09A9L6 caulobacter
26	227.5	7.1	351	2 093F47	093F47 pseudomonas
27	223	7.0	500	16 09KB49	09KB49 bacillus ha
28	216.5	6.8	463	16 09HXM7	09HXM7 pseudomonas
29	215.5	6.8	611	16 09PH14	09PH14 xylella fas
30	214	6.7	721	16 09PA43	09PA43 xylella fas
31	213	6.7	675	2 09KJ58	09KJ58 maritimonas
32	209	6.6	561	3 096MNO	096MNO bolyletis ci
33	205.5	6.4	635	3 09NKR0	09NKR0 leishmania
34	203.5	6.4	520	3 059944	059944 cerliporiops
35	203.5	6.4	591	10 09AUI2	09AUI2 pinus taeda
36	203	6.4	524	3 013422	013422 basidiomyc
37	202.5	6.3	565	10 09FRT5	09FRT5 arabidopsis
38	202	6.3	518	3 059896	059896 pycnopus
39	201.5	6.3	567	10 0941X2	0941X2 oryza sativ
40	199.5	6.3	533	3 060199	060199 pleurotus o
41	199	6.2	464	16 0920V6	0920V6 rhizobium m
42	197	6.2	463	2 08ROE2	08ROE2 lactococcus
43	197	6.2	518	3 09HDS9	09HDS9 polyorus c
44	197	6.2	605	16 08X525	08X525 raietonia s
45	196	6.1	352	2 093F57	093F57 pseudomonas

ALIGNMENTS

RESULT 1	PRELIMINARY	PRT	602 AA.
ID 09P8C3			
AC 09P8C3			
DT 01-OCT-2000 (TREMUREL. 15, Created)			
DT 01-OCT-2000 (TREMUREL. 15, Last sequence update)			
DT 01-JUN-2002 (TREMUREL. 21, Last annotation update)			
DE Polypheanol oxidase precursor.			
GN PROA.			
OS Acromonium murorum.			
OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;			
OC Hypocreales; Hypocreaceae; Mitosporic Hypocreaceae; Acromonium.			
OX NCBI_TaxID=45278;			
RP [1]			
RC SEQUENCE FROM N.A.			
RC SURAIN-CHS 157.72;			
RX MEDLINE=21268855; PubMed=11375170;			
RA Gouka R.J., van der Heiden M., Swarthoff T., Verrills C.T.;			
RT "Cloning of a phenol oxidase gene from Acromonium murorum and its			
RT expression in Aspergillus awamori."			
RL Appl. Environ. Microbiol. 67:2610-2616(2001).			
DR EMBL: AJ271104; CAB75422.1; -			
DR InterPro: IPR001117; Cu-oxidase.			
DR Pfam: PF00394; Cu-oxidase; 1.			
KW Signal.			
FT SIGNAL			
FT CHAIN			
SO SEQUENCE			
Query Match	53.58; Score 1705; DB 3; Length 602;		
Best Local Similarity	60.6%; Pred. No. 1.4e-122;		
Matches	325; Conservative 72; Mismatches 129; Indels 10; Gaps 4;		
QY	57 SPYNNLYRNAALIPPKOKMTITNPYCKDIWYIEIKPKQGRITPTLRATATGYD	116	
DB	65 SPAYT-LFQAPLSIPVKEPLFTVNTYNGEIDYIEIKHSQVFPPLGADLDGYD	123	
QY	117 GMSGPFENPVGCTETVVRFINNATVENSYHLGSPSRAPFDGMAEDVTPGCKYDYP	176	

Db 124 GTSPPPTIIOEGRSVVRFNKATVESSIHLSGFSRAPWDGMAEDVTNPGEEYDYYP 183
Qy 177 NYOSARLLMYHDHAFMKTAEANAYFGOAGAYIINDEADALGLPSGGEEDILITAKKY 236
Db 184 NAQAFRFSWYHDHAFMKTAEANAYFGOAGAYIINDEADALGLPSGGEEDILITAKKY 243
Qy 237 NADGFLRSTEGEDOLMGDVIHNGOAPMPEFLAVOCPKRRFRFLNAVSRAMILLYVRSS 296
Db 244 NSDGLTFSTGKGTQSLMGDVIQVNGVPMPEYFVEPRKRYFRLLDAVSRFSFLYFVTDAD 303
Qy 297 PVNRFPFOVIASDAGILAPVQTSNLYLAVEREIIIDFTNFACTOTDLRVANETNDG 356
Db 304 EDTRIKPFVVIASDGLSLEPERYTTSKLVLSIAERTIILDSDFEGKTIELRNEPVGGLG 363
Qy 357 DEDEYARTLEVRFRVYSSGTVB--DNSOVPSTLRDVPPEPKHKEGPAKHEFRSNGHYL 414
Db 364 IEVNDYDPTDKVRFVNAAGPLSSPDTSVYPSLRLDVPFPSSSTIIDHFRFRARAGOMS 423
Qy 415 INDVCFADYNEVNLAKPELGIYVEWLENSGSGSHPVHILVDRKILKRTG-----R 468
Db 424 INGTFESDVENLLANVPLGTVQVLQTLNAAQGMTHPIHILVDRKILSRGAATGATTR 483
Qy 469 GOVMPYESAGLKDVIYVLMGRGETLTLEAHYQPTGAYMNHCHNLIEDNDMAVFNVTAME 528
Db 484 G-VEPEESAGLKDVIYVLMGRGETLTLEAHYQPTGAYMNHCHNLIEDNDMAVFNVTAME 542
Qy 529 EKGVLQEDFEDPMKRAVRYNRDPFHARAGNFAESITARVOELAEQEPYRLD 584
Db 543 DYGVNSTALADPMQDEFRAPKPYDNDVEYRENAFSTDEIAEQVLQMASTLYPDND 598

RESULT 2

Q3M03 PRELIMINARY: PRT; 475 AA.
AC Q3M03;
DT 01-DEC-2001 (TREMBLrel. 19, Created)
DT 01-DEC-2001 (TREMBLrel. 19, last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, last annotation update)
DE Oxidoreductase-like protein.
GN AUR21.
OS Streptomyces aureofaciens.
OC Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
OC Actinomycetales; Streptomyces; Streptomycetaceae; Streptomyces.
OX NCBI_TaxID=1884;
RN [1]
RP SEQUENCE FROM N. A.
RC STRAIN=CCM3239;
RC Kormanec J., Bistakova J., Novakova R., Homeroova D., Rezuchova B.,
"Cloning and characterization of a new polyketide gene cluster in
Streptomyces aureofaciens CCM3239,"
Submitted (May-2001) to the EMBL/GenBank/DBJ databases.
EMBL: AY033994; AAK61713.1;
SEQUENCE 475 AA; 52602 MW; A2ED9A4C638D0C9 CRC64;

Query Match 19.2%; Score 612.5; DB 2; Length 475;
Best Local Similarity 34.3%; Pred. No. 1.1e-38;
Matches 174; Conservative 66; Mismatches 196; Indels 71; Gaps 21;
Qy 39 TEVFADSLAAGDDWESPYNLLYRNALPIPVYKOKMITNVTGDKIMYIEIKP 98
Db 21 SQAVASLATA-----EAPI-VFAHAMPFKULK-----TSTATSDL--YEIRMQE 67
Qy 99 FOQRIYPTLRATLVGDSGSPGTFFVNRGTETVVRFINNATYENSVHLGSPSRAPD 158
Db 68 AOVEIVKGLM-SKVTYDGTFFPPTIRATQGREVVVRRINELQVNTAVHLGHAHLSHD 126
Qy 159 GMADVFPFGKTYKQYIPNYOSARLLMYHDHAFMKTAEANAYFGOAGAYIINDEADALGL 218
Db 127 GLPMDTIVPGEERYRYRPNQPAASLWYHDHAFMKTAEANAYFGOAGAYIINDEADALGL 186
Qy 219 PSGGEEDILITAKKYNDGTLRSTEGEDOLMGDVIH--VNGOAPMPEFLAVOCPKRRYF 276
Db 187 PS--GPIVDVPLVINDARVADGTLITLRP-----SDCPHMLVNGKERPYFOVAAKRYF 238

Qy 277 RFLNAVSRAMILLYVTRSSPNVRIPFOVIASDAGILAPVQTSNLYLAVEREIIIDF 336
Db 239 RYNNACNANYVLRPAD-----GTFEQIGDGFLETPVOOSLMLGSRADIVDF 292
Qy 337 TNEACOTDLNRVAETNDVD-----EDEYARTL--EYMRVYSSGTYEDNSQVSTLRD 389
Db 293 SRY-----KVGDSVLEENPGQASIERPEVWRFDIVR-TAPDVSFVGRLL-- 335
Qy 390 VEPPEKGPADKHKFERNSNGHYLLINDGFADVNERYLAKPELGTVEWLEEN-----SS 445
Db 336 TTPYQPPPTVERDEI-RTFPAMTINGOSY-DPN-RDITAKLTITTEWYVRYNEAPAA 392
Qy 446 GG-----WSHPVHILVDFKILKRTGGRGVMPYESAGLKDVIYVLMGRGETLTIEAHYQ 499
Db 393 PGKPDFHLM-HSFHTHLTFYRLER--NGKRPAGTRDGLKOTVTLGPGDVIKIAMTGP 448
Qy 500 WTGAYMNHCHNLIEDNDMAVFNVT 526
Db 449 YTGQYLYHCHOLGHSNGGMRIDIVA 475

RESULT 3

Q8RMC6 PRELIMINARY: PRT; 431 AA.
AC Q8RMC6;
DT 01-JUN-2002 (TREMBLrel. 21, Created)
DT 01-JUN-2002 (TREMBLrel. 21, last sequence update)
DT 01-JUN-2002 (TREMBLrel. 21, last annotation update)
DE Jadz (Fragment).
GN JADZ.
OS Streptomyces venezuelae.
OC Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
OC Actinomycetales; Streptomyces; Streptomycetaceae; Streptomyces.
OX NCBI_TaxID=54571;
RN [1]
RP SEQUENCE FROM N. A.
RC STRAIN=ISP5230;
RC MEDLINE=21930291; PubMed=11932454;
RX Wang L., White R.L., Vining L.C.;
RT "Biosynthesis of the deoxyxysugar component of jadomycin B: genes in
the jad cluster of Streptomyces venezuelae ISP5230 for L-digitoxose
assembly and transfer to the angucycline aglycone,"
Microbiology 148:1091-1103(2002).
EMBL: AY026363; AAL82808.1;
DR NON_TER 431
FT 431
SEQUENCE 431 AA; 47033 MW; 867152A032D1A300 CRC64;

Query Match 16.1%; Score 513; DB 2; Length 431;
Best Local Similarity 33.8%; Pred. No. 4.2e-31;
Matches 155; Conservative 53; Mismatches 195; Indels 56; Gaps 16;
Qy 11 ASGLISGLVIGPMDGSHPIEAVDEVTETVFADSLAAGDDWESPYNLLYRNALPI 70
Db 21 ASGLISRTSL-SDTRAGPGAGSPFAQPVAAQAL-----APIYPTFTAPTI 68
Qy 71 PVPYKOKMITNVPYVGKDIWYEIEIKPQRIYPTLRATLVGDSGSPGTFFVNRPGT 130
Db 69 PVPARPVSTGTTD-----YSTPVQTTAEIIPGVATPVLT-YGGSFPGETIKARSGR 121
Qy 131 ETVVRFINNATYENSVHLGSPSRAPDGMADVTFPGGEYDYFPNYOSARLLMYHDH 190
Db 122 RVVYQAPRITTTGSMHLGAVVDPANCGPMDLITPGQRTYTPNPQVAAATLWYHDH 181
Qy 191 FMKTAENAYFGOAGAYIINDEADALGLPSGGEEDILITAKKYNDGTL-----RSTE 246
Db 182 HMEAEHYRGMSEGYLLISDNEALPLR--GYVDVIVVRDGLGNDGTLFFDHNTP 239
Qy 247 GEDODIMQDVIHNGOAPMPEFLAVOCPKRRFRFLNAVSRAMILLYVTRSSPNVRIPFOVI 306
Db 240 GRRS--WS-----TGKQPPYFOVAAKRYRLIILGNSMRP---EERLSDG---EFTQI 286
Qy 307 ASDAGLLOAPVQTSNLYLAVEREIIIDFTNF-AGOTLDRNV--AETNDVGDDEYAR 363

Db 287 ASRGLLPAPYTTTTLPLSPAERADIVDESRYPVSGSVYLENAFFEPEN----- 337
Qy 364 TLVEMF-VVSGTVEDNSOVPSTLRDVPPEPKKPGADKHFKFENSGHYLINDVGFAD 422
Db 338 -KEILRDVYRS--AANDPSSVPARLATLPPTAAPTQNRNTLDFDVGSGSIS--GKTW 392
Qy 423 VNERVLAKPELGTEVWELENSSGMSGSHPHILHNDPKI 461
Db 393 DEQRVDITVROGDEWELEIKNHPTFPHNFHILHVDRI 431

RESULT 4

Q9AMU4 PRELIMINARY; PRT; 582 AA.
AC Q9AMU4; 01-JUN-2001 (TREMBlrel. 17, Created)
DT 01-JUN-2001 (TREMBlrel. 17, Last sequence update)
DT 01-JUN-2002 (TREMBlrel. 21, Last annotation update)
Putative spore coat protein.
P0044F08.18 OR P0037C04.31.
Oryza sativa (Rice).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC Ehrhartoideae; Oryzeae; Oryza.
NCBI_TaxID=4530;

SEQUENCE FROM N.A.
RC STRAIN-CV. NIPPONBARE;
RA Sasaki T., Matsumoto T., Yamamoto K.;
RT "Oryza sativa nipponbare(GA3) genomic DNA, chromosome 1, PAC
clone:P0044F08.";
RL Submitted (NOV-2000) to the EMBL/GenBank/DBJ databases.
[2]
SEQUENCE FROM N.A.
RC STRAIN-CV. NIPPONBARE;
RA Sasaki T., Matsumoto T., Yamamoto K.;
RT "Oryza sativa nipponbare(GA3) genomic DNA, chromosome 1, PAC
clone:P0037C04.";
RL Submitted (FEB-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF002309; BAB2118.1; -
DR EMBL; AF003233; BAB5542.1; -
DR InterPro: IPR001117; Cu-oxidase.
DR InterPro: IPR002355; Multicopper oxidase.
DR Pfam: PF00394; Cu-oxidase; 1
DR PROSITE: PS00080; MULTICOPPER_OXIDASE2; UNKNOMN_1.
KW Coat protein.
SEQUENCE 582 AA; 64050 MW; B5054EECB2C5C1DA CRC64;

Query Match 15.6%; Score 497.5; DB 10; Length 582;
Best Local Similarity 27.3%; Pred. No. 1e-29;
Matches 111; Conservative 78; Mismatches 208; Indels 169; Gaps 26;

Qy 7 QLAASGLSGVLGIPMDTGSHPTEAVDPEKTEVPADSLAAGD-----DWESP- 59
Db 6 ELAVLLLVGVGA-----AGTRPPSAPP-----VREDTLQKVASLEMYVDELQPKI 55
Qy 60 YNLVYNNALPIPVYKQPKMITTPYVYKDWYIEIKPKPQOKIPLPRLATLVGDGMS 119
Db 56 YGFSMRHGHPSP-----IRLTIGMYOK-KWKFHRDL-----PASTVVFVGTS 96
Qy 120 -----PGTFNVPKGTETVVRFIN-----NATVNSVHLHGSPS 153
Db 97 AATATPFGPIIEAAGVPLSVYQNTLPAHILPMDPTVTALPRRGVPTVYVHLHGGAH 156
Qy 154 RAEFDG-----MAEDVTPGEYKD-----YFPYOSARLLWYHDAFMKTAENAYF 200
Db 157 PQGDSARAFM-----FTAGFGETGPAWSTPTTYTYPNAQSPGLWYHDAHGLRANLLA 211
Qy 201 GQAGATYINDEADA-LGIPSGYGEFDIPILITAKYNNADGTLRST-----EGEDQ 250
Db 212 GLGAYVIRNPFAVEAPLGLPCG--DEFDRLMLADRSFYADGSITYMNTGITIPIHQPMP 270

Qy 251 DLMGDIVHNGOWPFPFLNVOPRKRYRFRFLNAASRAWLLYVRTSPNVRIPROVJASDA 310
Db 271 EYGEALITVNGKAMPFLAVARRRFRRLINTSNARKYNNLSITN-----GIPTVGSDF 324
Qy 311 GLLOAPVQTSNLYLAVEREIIIDFTNFAQOTLDLRNVA-----ETNDVGDEDEYA 362
Db 325 NYLSKPYTASLAVSAVEFDVYVDFQSGTSSSEALVNTAPYPYPDQGANDLNG----- 379
Qy 363 RTLEVMPFVVSSTVEDNSOVPSTLRDVPPEPKKPGADKH--FKTE-RSNG---HYLI 415
Db 380 ---KVMKFVISPAKAKDTSRPVAKLDYVAVEEAQVORYIWAYEEDATGNPTHLXI 436
Qy 416 NDVGFADVNERVLAKPELGTEVWELENSSGMSGSHPHILHNDPKIKRG----- 466
Db 437 NGRLED---PATETPRPGTTEWEVINTLPD-NHPLHLATFOATRVGLDEDAFKG 492
Qy 467 -----GRGOVMPYESAGIKDVYMLRGSETLTI----- 493
Db 493 CMKLANDAVRCNYSRAVAGEVAPEBEKGMKNVYKLAQYMTIYVKKFFMVDSGRPYF 552
Qy 494 EAHYQPTGAYMMHCHNLHEDNDM 519
Db 553 DATAEP---GYVYHCHILDEHDNMI 575

RESULT 5

ID 023123 PRELIMINARY; PRT; 568 AA.
AC 023123;
DT 01-JAN-1998 (TREMBlrel. 05, Created)
DT 01-JAN-1998 (TREMBlrel. 05, Last sequence update)
DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
DE F19G10.5 protein.
GN F19G10.5.
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eustosids II; Brassicales; Brassicaceae; Arabidopsis.
NCBI_TaxID=3702;

SEQUENCE FROM N.A.
RC STRAIN-CV. COLUMBIA;
RA Federici N.A., Palm C.J., Conway A.B., Kurtz D.B., Conway A.R.,
Au M., Araujo R., Buehler E., Dewar K., Feng C., Li Y.,
Ojima O., Osborne B.J., Shinn P., Sun H., Toriumi M., Vytaske A.V.,
Yu G., Ecker J., Theologis A., Davis R.W.;
RL Submitted (APR-1997) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF000657; AAB72167.1; -
DR InterPro: IPR001117; Cu-oxidase.
DR Pfam: PF00394; Cu-oxidase; 1
SEQUENCE 568 AA; 64355 MW; C4314C889576E35E CRC64;

Query Match 15.1%; Score 480; DB 10; Length 568;
Best Local Similarity 28.0%; Pred. No. 2.2e-28;
Matches 146; Conservative 78; Mismatches 167; Indels 130; Gaps 20;

Qy 109 PATLVGYDGM-----PGTFNVPKGTETVVRFIN-----AT-----V 142
Db 71 PATTVAYVYGTSSKAKATVPPTIETVYGVVDYVYVNRHLPRSHILPMDPTISPATPKHGI 130
Qy 143 ENSVHLHGSPSRAPFDGMADVTPEGEYKD-----YFPYOSARLLWYHDAFMK 193
Db 131 PTYVHLHGSGIHEPTSDGNA-DANFTAGFRETGKRWKTTTLHYENKQDPGMWYHDAHML 189
Qy 194 TAENAYFGQAGAYTINDEA-EDALGIPSGYGEFDIPILITAKYNNADGTL-RSTEGEDD 251
Db 190 TVNNLLAGLVAYILRHHAIVESPQLPTG-DEFDRLIIPDRSPKDGSIYMATGNPS 248
Qy 252 L-----WGVYHNGOWPFPFLNVOPRKRYRFRFLNAASRAWLLYVRTSSPNRIRP 303
Db 249 IHPQOWPEYGVDAIYVNGKAMPRLNVRRRRYRRLINASNAREFFKFF-----SNGLDF 302
Qy 304 OVIASDAGLLQAPVQTSNLYLAVEREIIIDFTNFAQOTLDLRNVA-----ETNDVGDE 358

Db	86	PATPVAYGTSKRSAATVP	PGPTIEAYGVYDVTWVNHNLPLHIIHLPMDPTISPAIRKAGGI	145
Qy	143	ENSVTHHGSPSRNAP	PDGNAEDVTFPGCEKD-----YFPVYQASARLLMTHDNAFMK	193
Db	146	PTVYVHLHGSIHEPTSDGNA	-DSWFAAGKEGSKTKTKTTHYANKQDGNMHHDDHAAGL	204
Qy	194	TAENAFGCGACAYII	-NDEAEDALGPGSGEFDIPLLTAKYNNADGLT-RESGED--	249
Db	205	TRNNILAGLGSLYILRHSSVESPLPLPG	-REFQDPLVTPRSPRKXGSIYMNATGNPT	263
Qy	250	-----ODIMGVIVHNGQ	PFPELVNVDPRKTRFREFPLAANAARMLLYLVRTSPNNRIPF	303
Db	264	IHPQWPEYFGGAIIVNGK	AMPRLTVRRKKRFRRTINASNAFRFFEFF-----SNGIDF	317
Qy	304	OYVASAGLQAPVOTS	NLYLAVAREYELIIDFTNFGQTLDELNNVAETNDVGDGEYAR	363
Db	318	IYVSDSASVLAAPVSTKSV	LYALPSIYDVLDVDFSKSTKAILLNNAAPYPPSGDPVTEE	377
Qy	364	TLEVMRFVSSGTVEDNS	QVSTPLDVPFPHKEGPADKHF--KFEESNG----HYLIN	416
Db	378	NSKVMKFIINTYKSEVDTS	IIIPKLTIEP-PAHVSTSPSTRYIAEFYVSSIDEPTHLYIK	436
Qy	417	DVGFADVNRVYLAKE	LGVEVWELENSGGSHPVHILYDFKILRTG-----	466
Db	437	GLPY--	-NAPVTEPKIGTSEWEVEMINTED-NHPLHILGLFVLBDOTALVNSSEETEC	492
Qy	467	-----	-GRGVMPYESAGLKVY-----MIGRGETLTIE	494
Db	493	MKRRNDVAVCELSK	ARGCKKTAIVYHNEGKMYKRMKGHTKTLVFSYIHSNESISFD	552
Qy	495	AHYQWGTAYVMHCHNL	IHEDNMAYF	522
Db	553	ATQEP--	-GYVYCHILDHEDNMAMRP	577
RESULT 9				
Qy	09C9A4	PRELIMINARY;	PRT;	591 AA.
Db	09C9A4	01-JUN-2001 (TREMBLrel. 17, Created)		
Qy	09C9A4	01-JUN-2001 (TREMBLrel. 17, Last sequence update)		
Db	01-JUN-2002 (TREMBLrel. 21, Last annotation update)			
Qy	09C9A4	230920.3.		
Db	09C9A4	Arabidopsis thaliana (Mouse-ear cress).		
Qy	09C9A4	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;		
Db	09C9A4	Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;		
Qy	09C9A4	eucosids II; Brassicales; Brassicaceae; Arabidopsids.		
Db	09C9A4	NCBI_TaxId=3702;		
Qy	09C9A4	SEQUENCE FROM N.A.		
Db	09C9A4	STRAIN=CV. COLUMBIA;		
Qy	09C9A4	MEDLINE=21016719; PubMed=11130712;		
Db	09C9A4	Theologos A., Ecker J.R., Palm C.J., Federspiel N.A., Kaul S.,		
Qy	09C9A4	White O., Alonso J., Altafi H., Araujo R., Bowman C.L., Brooks S.Y.,		
Db	09C9A4	Buehler E., Chan A., Chao Q., Chen H., Cheuk R.F., Chin C.W.,		
Qy	09C9A4	Chung M.K., Conn L., Conway A.B., Conway A.R., Creasy T.H., Dewar K.,		
Db	09C9A4	Dunn P., Eguu P., Feldblum T.V., Feng J.-D., Fong B., Fujii C.Y.,		
Qy	09C9A4	Gill J.E., Goldsmith A.D., Haas B., Hansen N.F., Hughes B., Hulzer L.,		
Db	09C9A4	Hunter J.L., Jenkins J., Johnson-Hopson C., Khan S., Khaykin E.,		
Qy	09C9A4	Kim C.J., Koo H.L., Kremetskaia I., Kritz D.B., Kwan A., Lam B.,		
Db	09C9A4	Langin-Hooper S., Lee A., Lee J.M., Lenz C.A., Li J.H., Li Y.-P.,		
Qy	09C9A4	Lin X., Liu S.X., Liu Z.A., Luros J.S., Maiti R., Marzilli A.,		
Db	09C9A4	Miltschker J., Miranda M., Nguyen M., Nieman W.C., Osborne B.I.,		
Qy	09C9A4	Pai G., Peterson J., Pham P.K., Rizzo M., Rooney T., Rowley D.,		
Db	09C9A4	Sakano H., Salzig S.L., Schwartz J.R., Shinn P., Southwick A.M.,		
Qy	09C9A4	Sun H., Tallon L.J., Tambunga G., Toriumi M.J., Town C.D.,		
Db	09C9A4	Utechtack T., Van Aken S., Vaysberg M., Vysotskaya V.S., Walker M.,		
Qy	09C9A4	Wu D., Yu G., Fraser C.M., Venter J.C., Davis R.W.,		
Db	09C9A4	"Sequence and analysis of chromosome 1 of the plant Arabidopsis		
Qy	09C9A4	thaliana."		
Db	09C9A4	Nature 408:816-820(2000).		
Qy	09C9A4	EMBL; AC016972; AAG51692.1;		
Db	09C9A4			

DR InterPro: IPR001117; Cu-oxidase.
DR Pfam: PF00394; Cu-oxidase; 1.
KW Coat protein.
SQ SEQUENCE 591 AA; 67358 MW; B0CE7BB0E8F05AAF CRC64;
Query Match 14.1%; Score 450; DB 10; Length 591;
Best Local Similarity 27.4%; Pred. No. 4.8e-26;
Matches 142; Conservative 74; Mismatches 182; Indels 120; Gaps 18;
QY 109 PATLVGYDGM-----GPTFENVRGTEYVVFRTIN-----NMTV 142
DB 86 PATFPAVGTSTKRSKSTVPCPTTEAVYGVDTVTWNNHLPLHLIPLMDPTISPATIKKGT 145
QY 143 ENSVHLHGSPSPAPFDGMAEDVTFPEYKD-----YFPPNYSARLWYHDAFAFK 193
DB 146 PTVVHLHGCIHEPTSDGNA-DSMFTAGFKETGSKTKKTHYVNNQOGNNMYHDAAGL 204
QY 194 TAEKAVFGQAGYII-NDEADALGLPSGCGFDIPLITAKYNAADGL-RSTGED-- 249
205 TRVNLLAGILGSIYILRHSSVSPLRLPTG-REFDPLVIFDRSFRKDSIYNNATGNMPT 263
250 -----ODLMGDVHVNGOPMPELVNVPKRYFRFLNNAVSRAWLLYLVRTSSPNVRIPE 303
DB 264 IHPQMPREYFGALITVNGKAMPRLVRRKRYFRITMASNAFFRFF-----SNGIDF 317
QY 304 QVITASDAGILAPVQTSNLYLAVEREIIIDFTNFAQOTLDLRNVAETNDVGDDEXAR 363
DB 318 IVVGSDSAYLAKPVSTKSVLLAPSEIVDLVDFSKSTKALIANAPYPSPGVTEE 377
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DB 378 NSKWKFTINKSEVDTSIIIPKLIETP-PAHVSTSTRTRYAMEYVSSIDEPTHLIN 436
QY 417 DVGFDVVERVYLAKEPELTVE-----VMELENSSGSHVHILVDFKILKRTG 466
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QY 467 -----GRGOVMPYESAGLKDV-----W 484
DB 493 LVKSEEFTECMTRNDVAKCEISKYARGNKTAVTHERGMKNVFMGMFGVTKILVRSY 552
QY 485 LGRGETLITLTAHYQWPTGAYMWHCHNLHEDNDMAVF 522
DB 553 IHSNESYSFDAQEP---GYVYHCHILDHEDMMMRPF 587
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067206 PRELIMINARY: PRT: 527 AA.
067206:
01-AUG-1998 (TREMBLrel. 07, Created)
01-AUG-1998 (TREMBLrel. 07, Last sequence update)
01-MAR-2002 (TREMBLrel. 20, Last annotation update)
DE Periplasmic cell division protein (SUF1).
CN SUF1 OR AO_1130.
OS Aquifex aeolicus.
OC Bacteria; Aquificae; Aquificales; Aquificaceae; Aquifex.
OX NCBI_TaxID=63363;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=VF5;
RA MEDLINE=98196666; PubMed=9537320;
RA Deckert G., Warren P.V., Gaasterland T., Young W.G., Lenox A.L.,
RA Graham D.E., Overbeek R., Sneed M.A., Keller M., Aujay M., Huber R.,
RA Feldman R.A., Short J.M., Olson G.J., Swanson R.V.;
RT "The complete genome of the hyperthermophilic bacterium Aquifex
aeolicus".
RL Nature 392:353-358(1998).
DR EMBL: AE000724; AAC07157.1;
DR InterPro: IPR001117; Cu-oxidase.
DR InterPro: IPR002355; Multicu_oxidase2.
DR Pfam: PF00394; Cu-oxidase; 1.
DR PROSITE: PS00080; MULTICOPPER_OXIDASE2; 1.

KW Cell division; Complete proteome.
SQ SEQUENCE 527 AA; 59490 MW; F361BF791FF97355 CRC64;
Query Match 13.8%; Score 439.5; DB 16; Length 527;
Best Local Similarity 30.1%; Pred. No. 2.6e-25;
Matches 147; Conservative 72; Mismatches 191; Indels 79; Gaps 21;
QY 98 PQQRITPLRPATLVGYDGMSP-----GPTFENVRGTEYVVFRTINATVENSU 146
DB 58 PDGQGVSTAKMTTLEVIIPKSTDLVYEIDNEYPIVFLKRGQFFSADFVNNSEDSII 117
QY 147 HLHGSPSPAPF--DGMADVTFPGYKTYFPNT--OSARILMTYHDAFMKTAENAYFG 201
DB 118 HWHG--FRAPMKSDCHPYRAYVGDG--TYSYDFDTIIRSGTYFHPHGHGTGYQVYVG 173
QY 202 QAGAVIINDEADAL--GLPSGCGFDIPLITAKYNAADGLRSTEGEDDOLMGDVIVH 259
DB 174 LAGMTIIEDEDEDKQALDLEYGVIDIPLIIQDKTFPSSGQLYNNPGHMGFMQDITLV 233
QY 260 NGQMPFLNVOPKRYFRFLNNAVSRAWLLYLVRTSSPNVRIPEQVIASDAGLLQAPVQT 319
DB 234 NLTFRPYMDVERKIRFRILNGSNAPRYRALLR--GNQRRFVWIGVEGGLDTPREV 290
QY 320 SNLYLAVEREIIIDFT-----NFAQTLDL-----RNAETN--- 353
DB 291 NEILVAPGERIDIIVDFDASVNDVYIKLYNPPHNLIGMIGMRMGMEGMRGNGMN 350
QY 354 -DVG--DDEVARITLEVRFVYVSGTVDNSQVSTLDVPPPHKEPADKHFEKERSN 410
DB 351 MDGMADNSEF-----EVMERFVTKDSAYDKS-IPRLSEVT-PINTDAQOVRITLGMRR 404
QY 411 GHYLIN---DVGFPA--DVNE-RYLARPELTGVEWELSENSSGSHVHILVDFKIL 462
DB 405 MVFTINGETWEDGYANPDQINNPKVLFQNNQNDVYIIEYVNTGMV-HPMHLHGQFQVL 463
QY 463 KRTGGRGOVMPYESA--GLKDVYVILGRETTLIE--AHQDPTCAIYMHCHNLHEDND 517
DB 464 ERSIG-----PLRATDGMKDTVIYAPMETVRIADVMSHPNEHQIYLLHCHILHDEG 518
QY 518 MAAVENYTA 526
DB 519 MAAVTRVNA 527
Search completed: July 1, 2003, 10:41:00
Job time : 91 secs

GenCore version 5.1.6
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6388329

OM protein - nucleic search, using frame_plus_p2n model

Run on: July 3, 2003, 22:08:06 ; Search time 4358 Seconds

(without alignments)
3966.743 Million cell updates/sec

Title: US-10-080-233-2

Perfect score: 3189

Sequence: 1 MLFMSQLAASGLSLGVLG.....AEOPEYRLDEILEDGIEE 594

Scoring table:

BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 2054640 seqs, 14551402878 residues

Total number of hits satisfying chosen parameters: 4109280

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Command line parameters:

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-Q-cgn2_1/uspt0.spool/US10080233/runat_01072003_094519_26096/app.query.fasta_1.775
-DB-GenEmbl -QFMT-fastap -SUFIX-rige -MINMATCH-0.1 -DOOPCL-0 -DOOPEXT-0
-UNITS-bits -START-1 -END-1 -MATRIX-blosum62 -TRANS-human40.cdi -LIST-45
-DOCALLIGN-200 -THR.SCORE-pct -THR.MAX-100 -THR.MIN-0 -ALIGN-10 -MODE-LOCAL
-OUTFMT-pto -NORM-ext -HEAPSIZE-500 -MINLEN-0 -MAXLEN-200000000
-USER-us10080233.gcgn_1_1.2819-rcunat_01072003_094519_26096 -NCPU-6 -ICPU-3
-NO_MAP -LANGBOUERR -NEG.SCORES-0 -WAIT -DSPBLOCK-100 -LONGLOG
-DEV_TIMEOUT-120 -WARN_TIMEOUT-30 -THREADS-1 -XGAPOP-10 -XGAPEXT-0.5 -FGAPOP-6
-FGAPEXT-7 -YGAPOP-10 -YGAPEXT-0.5 -DELOP-6 -DELEXT-7

Database :

GenEmbl: *
1: gb_hlg: *
2: gb_hlg: *
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9: gb_pr: *
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13: gb_ro: *
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17: em_da: *
18: em_hum: *
19: em_hum: *
20: em_hum: *
21: em_or: *
22: em_or: *
23: em_ov: *
24: em_ov: *
25: em_ph: *
26: em_ph: *
27: em_ro: *
28: em_ro: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
29	3189	100.0	1791	6 AR211556	AR211556 Sequence
30	3165	99.2	7259	6 AX384798	AX384798 Sequence
31	3056	95.8	3672	6 AR211554	AR211554 Sequence
32	1870	58.6	2063	6 AR211555	AR211555 Sequence
33	1868	58.6	2905	6 AR211555	AR211555 Sequence
34	1724.5	54.1	1942	8 MYRBOR	D12579 M. verrucar
35	1724.5	53.6	2126	6 E05283	E05283 B. litoralis
36	1708.5	53.6	2126	6 AMU271104	AMU271104 Acremoniu
37	1620.5	50.8	1958	6 AR122996	AR122996 Sequence
38	1620.5	50.8	1958	6 AX101096	AX101096 Sequence
39	1620.5	50.8	1958	6 AX108672	AX108672 Sequence
40	1620.5	50.8	1958	6 AX456852	AX456852 Sequence
41	1620.5	50.8	2095	6 AR122997	AR122997 Sequence
42	1620.5	50.8	2095	6 AX101098	AX101098 Sequence
43	1620.5	50.8	2095	6 AX108674	AX108674 Sequence
44	1620.5	50.8	2095	6 AX456854	AX456854 Sequence
45	1540.5	48.3	3241	8 MYRBOR	D14081 M. verrucar
1	713	22.4	16585	1 BS007638	BS007638 Bacillus
2	694.5	21.8	1470	6 BS008004	BS008004 Bacillus
3	666.5	20.9	858	6 AX433789	AX433789 Sequence
4	588	18.4	109519	6 AX195929	AX195929 Sequence
5	519	16.3	2302	1 SAPHSA	U04283 Streptomyce
6	516.5	16.2	3446	6 AX204969	AX204969 Sequence
7	513	16.1	12543	1 AY026363	AY026363 Streptomy
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9	500	15.7	1614	6 AX065821	AX065821 Sequence
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RESULT 1

ALIGNMENTS

AR211556
LOCUS AR211556 1791 bp DNA linear PAT 20-JUN-2002
DEFINITION Sequence 5 from patent US 6399329.
ACCESSION AR211556
VERSION AR211556.1 GI:21514909
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE
1 (bases 1 to 1791)
AUTHORS Wang, H. and Bodie, E.A.
TITLE Phenol oxidizing enzymes
JOURNAL Patent: US 6399329-A 5 04-JUN-2002;
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Location/Qualifiers
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source
BASE COUNT 380 a 551 c 451 g 409 t
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Seq. No.: 1.04e-247 Length: 1791
Score: 3189.00 Matches: 594
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Best Local Similarity: 100.00% Mismatches: 0
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QY 21 IleProMetAspThrGlySerHisProIleGluAlaValAspProGluValLysThrGlu 40
DB 67 ATCCGAGTGAACACGGGAGCCACCCCATGAGCTGTGATCCGAGTGAAGCTGAG 126
QY 41 ValPheAlaAspSerLeuLeuAlaAlaLysAspAspAspTrpGluSerProProTyr 60
DB 127 GTCCTCGCTGACCTCCCTCTGTCGACAGCGGCTGACGAGTGGAGTCACTCCATAC 186
QY 61 AsnLeuLeuTyrArgAsnAlaLeuProIleProProValLysGlnProLysMetIle 80
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QY 241 ThrLeuArgSerThrGlyGlyGluAspGlnAspLeuTyrGlyAspValIleHisValAsn 260
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VERSION	AX384798.1	GI:19577933	
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SOURCE	unidentified.		
ORGANISM	unidentified		
REFERENCE	1		
AUTHORS	Hood, E., Howard, J.A., Bailey, M., van Gastel, F.J., Ward, M., Wang, H. and Woodard, S.		
TITLE	Method of increasing recovery of heterologous active enzymes produced in plants		
JOURNAL	Patent: WO 0196543-A 3 20-DEC-2001;		
ATTRES	Prodigene, Inc. (US); Genencor, Inc. (US)		
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ORIGIN			
Alignment Scores:			
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Score:	3165.00	Matches:	593
Percent Similarity:	99.66%	Conservative:	1
Best Local Similarity:	99.50%	Mismatches:	0
Query Match:	99.25%	Indels:	0
DB:	6	Gaps:	0
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Qy	21	IllePrometaSPThnglySerHisProileGluValAlaSPProGluValLysThnglu	40
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Qy	81	ThrasnProValThnglyLysAspIleTTrTyTgIuileGluileLysProPheGln	100
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Qy	161	AlaGluAspValThrPheProGlyGluTyTlysAspTyTTrPheProAsnTyGlnSer	180
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QY	440	IuLeuGluAsnSerSerGlyIleTyrTrpSerHisProValHisIleHisLeuValAspPheL	460
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QY 540 IOMELASNPRLYSTPARGALALVALPROTYRASNARGASNPHEHISALARGALAG 560
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DB 6827 CCATTAACCCCAAGGCGCGCGCTTCTTACAAACCGACACTTCCATGCTCCGCTG 6886
QY 560 IYASNPHESEALAGLUSERLIERHIALARGVALGLNLEUALAGLUNGUPROT 580
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DB 6887 GAACATCTCCGCGAGTCATCACTACTGCCGAGTCCAGAGCTGCCAGCAGGAGCGGT 6946
QY 580 YRASNPARGLEUASPGLIILEUGLUSASPLEUGLYIILEUGLU 594
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DB 6947 ACAACCGCTCGATGAGATCTCGAGGATCTTGCAATGAGAGAG 6990
RESULT 3
AR211554 3677 bp DNA linear PAT 20-JUN-2002
LOCUS AR211554
DEFINITION Sequence 1 from patent US 6399329.
ACCESSION AR211554
VERSION AR211554.1 GI:21514906
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 3677)
AUTHORS Wang, H. and Bodle, E. A.
TITLE Phenol oxidizing enzymes
JOURNAL Patent: US 6399329-A 1 04-JUN-2002;
FEATURES Location/Qualifiers
source 1. 3677
/organism="unknown"
BASE COUNT 822 a 1057 c 849 g 948 t 1 others
ORIGIN
Alignment Scores:
Pred. No.: 1.36e-236 Length: 3677
Score: 3056.00 Matches: 593
Percent Similarity: 86.70% Conservative: 0
Best Local Similarity: 86.70% Mismatches: 1
Query Match: 95.83% Indels: 91
Gaps: 5
DB: 6
US-10-080-233-2 (1-594) x AR211554 (1-3677)
QY 1 MetleuphelysSerTrpGlnleuAlaAlaAserylLeuSerGlyValleugly 20
DB 1044 ATGCTGTCAAGTATGCAACTGGCAGACCTCCGGCTCTGTCGAGTCTCGGC 1103
QY 21 IlePrometAspThrGlySerHisProIleGluAlaValAspProGluValLysThrGlu 40
|||||
DB 1104 ATCCGATGACACCGGACGCCACCCCAATGAGCTGTGATCCCGAAGTGAAGACTGAG 1163
QY 41 ValPheAlaAspSerLeuLeuAlaAlaAlaGlyAspAspTrpGluSerProTyr 60
DB 1164 GTCTTCGCTGACTCCCTCTTGTGTCAGACAGGCGATGACGATGACCTCCATAC 1223
QY 61 AsnleuLeu-----Tyr 64
|||||
DB 1224 AACTTGTCTTACAGGTGAGACACCTGTCACCTGTTTCCCTGATTAACCTTAT 1283
QY 65 ArgAsnAlaLeuProIleProProValLysGlnProLysMet----- 78
|||||
DB 1284 AGGAATGCCCTGCAATTCACCTGTCTCAAGACGCCCAAGATGATGTGTTGAAATTTCTA 1343
QY 79 -----IleIleThrAsnProValThrGlyLy 87
|||||
DB 1344 CGAAGCAACTCGGCCCGCACTAATGATTTATAGATCTTTACCAACCTGTCCACGGCAA 1403
QY 87 SASPIETrPTrYrGluIleGluIleLysProheGlnArg----- 102
|||||
DB 1404 GGACATTTGTACTATGATGATGATCAACGCAATTCACGAAAGGAGTGTGCTCAG 1463
QY 103 -----IleTyrProThrLeuArgPr 109
|||||
DB 1464 AAACCTGTGTAAATTAATCATTTGTACTGACCTTTTCAGATTTACCCACCTTGCGGCC 1523

QY 109 OAlaThrLeuValGlyTyrAspGlyMetSerProGlyProThrPheAsnValProArgG1 129
|||||
DB 1524 TGCCACTCTCGTCGGCTACGATGGCATAGCCCTGCTCTACTTTCATGTTCCACAGAG 1583
QY 129 YThrGluThrValAlaArgPheIleAsnAsnAlaThrValGluAsnSerValHisLeuH1 149
|||||
DB 1584 AACAGAGACTAGTATGATTCATCAACAAAGCCACCTGGAGAACTGCTGCATCTGCA 1643
QY 149 SGlySerProSerArgAlaProPheAspGlyThrAlaGluSpsValThrPheProGlyG1 169
|||||
DB 1644 CGGCTCCCATCGCGTCCCTTTCGATGATGTGGGCTGAAGATGAGACTTCCCTCGCGCA 1703
QY 169 UTyrlLysAspTyrrTyrrPheProAsnTyrrGlnSerAlaArgLeuLeuTrpYrHisAspH1 189
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DB 1704 GTACAGAGATTAACACTTCTCCCACTACCAATCCGCCCTTCTGTGTGATCACTGACCA 1763
QY 189 sAlaPheMetLys----- 193
|||||
DB 1764 CGCTTTCATVGA--GGTATGCTACGAGCCTTATCTTCTGTGCTAACCTTTGGCTAACCA 1822
QY 194 -----ThrAlaGluAsnAlaTyrPheGlyGlnAlaGlyAlaTyrrIleLeas 209
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DB 1823 CTTCCTTTCGTAGACTGCTGAGAAATGCTTACTTGTGTCAGGCTGCGCTACATTATCA 1882
QY 209 nAspGluAlaGluAspAlaLeuGlyLeuProSerGlyTyrrGlyLupheAspIleProle 229
|||||
DB 1883 CGACGAGCTCAGAGATGCTCGGCTTCCTGATGAGGCTATGCGAGTTCGATTCCTGCT 1942
QY 229 uIleLeuThrAlaLysTyrrTyrrAsnAlaAspGlyYThrLeuArgSerThrGluGluAs 249
|||||
DB 1943 GATCCTGACGCCCAAGTACTATTAACGCCGATGATGATACCTCGCTGACCGCGGGGTGAGA 2002
QY 249 pGlnAspLeuTrpGlyAspValIleHisValAsnGlyLupProTrpPheLeuAsnVa 269
|||||
DB 2003 CCAGGACCTGTGGGAGATGTCATTCATGTAAGCGAGACGACGATGCTTCTTAACT 2062
QY 269 IGluproArgLysTyrrArgPheArgPheLeuAsnAlaAlaValSerArgAlaTrpLeu 289
|||||
DB 2063 CCAGCCCGCAAGTACGCTTCCGATTCCTCAAGCGTCCGCTGCTGCTGGCTGCT 2122
QY 289 uTyrlLeuValLarghrSerSerProAsnValArgIleProheGlnValIleAlaSerAs 309
|||||
DB 2123 CTACCTGCTCAGGACACCTCTCCCAACGTGAGATTCCTTCCAAAGCATTTGCTCTGA 2182
QY 309 pAlaGlyLeuLeuGlnAlaProValGlnThrSerAsnLeuTyrrLeuAlaValAgluAr 329
|||||
DB 2183 TGTGTGCTCTTAAGCCCCCGTTCAAGCTCTTAACCTTAACCTGCTGTGCGGAGCG 2242
QY 329 gTyrrGluIleIlele----- 334
|||||
DB 2243 TTACGAGATCAATTTATGATAGCCCTCCCTCCATCAAGATGATCAAGAACTTAAGACT 2302
QY 335 -----AspPheThrAsnPheAlaGlyGlnThrLeuAspLeuArgAsnValAlaG1 351
|||||
DB 2303 AACACTGTGTAACTTCCCAACTTGTCTGGCGCAACACTTGTACCTGGCGCAACGTTGTGA 2362
QY 351 uThrAsnAspValGlyAspGluAspGluTyrrAlaArgThrLeuGlnValMetArgPheVa 371
|||||
DB 2363 GACCAAGATTCGCGCGACGAGATGAGTACGCTCGCACTTCCAGGTGATGCCCTTCTGT 2422
QY 371 lValSerSerGlyThrValGluAspAsnSerGlnValProSerThrLeuArgAspValPr 391
|||||
DB 2423 CGTCAGCTGTGCACTGTGAGCAACAAGCAGAGCTCCCTCCACTCGTGCAGCTTCC 2482
QY 391 oPheProProHisLysGluGlyProAlaAspLysHisPheLysPheGluArgSerAsnG1 411
|||||
DB 2483 TTTCCTCTCCACACAAGAGAGCCCGCGCAACACTTCAAGTTTAAAGCAGCAACAGG 2542
QY 411 yHisTyrrLeuLeuAsnSpsValGlyPheAlaAspValAsnGluArgValleuAlaLysPr 431
|||||
DB 2543 ACCTTACCTGATCAACGATGTGGCTTGGCGATGTCAATGAGCGTGTCTGCGCAAGCC 2602

QY 431 ogileuGLyThrValGluValTrrpGluLeuGluAsnSerSerglyLysThrSerHispr 451
|||||
Db 2603 CGAGCTCGGACCGCTTGAAGTCTGGAGAGCTCGAAGTCTCTGGAGGCTGGAGACACC 2662
QY 451 ovalHisIleHisLeuValAspPheLysIleLeuLysArgThrGlyLysArgLysIleVal 471
|||||
Db 2663 CGTCCACATTCACCTGTTGACTTCAAGATCTCCAAACGAACTGGTGGTGGCCAGGT 2722
QY 471 lmetProTyrGluSerAlaGlyLeuLysAspValValTrrpLeuGlyArgLysIleThrLe 491
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Db 2723 CAGTCCCTACGAGTCTCTGCTCTTAAAGATGTCGTGGTGGGAGGGGTGAGACCT 2782
QY 491 urHrIleGluAlaHisIleTyrGlnProTrrpThrGlyAlaTyrMetThrPheLysHisAsnLe 511
|||||
Db 2783 GAGCATGAGAGGCCACAGACACCTGGAGCTGAGCTTACATGGAGACGTCCAAACCT 2842
QY 511 uIleHisGluAspAsnAspMetMetAlaValPheAsnValThrAlaMetGluLysGly 531
|||||
Db 2843 CATTCACAGAGATACGACATGATGCTGTATTCACAGCTCACGCCCATGAGAGAGAGG 2902
QY 531 YTrIleuGlnGluAspPheGlnAspPheMetAspProLysTrrpArgAlaValProTyrAs 551
|||||
Db 2903 ATATCTCAGAGAGACTTGAAGAGACCCATGAAACCCAGAGTGGCGCTTCCTTACAA 2962
QY 551 nArgAsnAspPheHisAlaArgAlaGlyAsnPheSerAlaGluSerIleThrAlaArgVal 571
|||||
Db 2963 CGGCAACGACTTCCATCTCGCGCTGGAACCTTCGCGCGAGCCATCTACCTGCCAGT 3022
QY 571 lGlnGluLeuAlaGlnGluLysProTyrAsnArgLeuAspGluIleLeuGluAspLeuGly 591
|||||
Db 3023 GCAGAGCTGCGCGAGAGAGAGCGGTACAAACCGCTCGATGATCTCGAGATCTTGG 3082
QY 591 YTrIleGluLys 594
|||||
Db 3083 ATTCAGAGAG 3092

RESULT 4
AR211557 2063 bp DNA linear PAT 20-JUN-2002
LOCUS AR211557
DEFINITION Sequence 6 from patent US 6399329.
ACCESSION AR211557
VERSION AR211557.1 GI: 21514910
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 2063)
AUTHORS Wang, H. and Bodie, E.A.
TITLE Phenol oxidizing enzymes.
JOURNAL Patent: US 6399329-A 6 04-JUN-2002;
FEATURES
source location/Qualifiers
1..2063
source /organism="unknown"

BASE COUNT 501 a 604 c 510 g 448 t
ORIGIN
Alignment Scores:
Pred. No.: 2,47e-141 length: 2063
Score: 1870.00 matches: 365
Percent Similarity: 67.62% conservative: 82
Best Local Similarity: 55.22% mismatches: 133
Query Match: 58.64% indels: 82
DB: 6 gaps: 11

US-10-080-233-2 (1-594) x AR211557 (1-2063)

QY 2 LeuphelySerTrpGlnLeuAlaAlaAlaSerGlyLeuLeuSerglyValLeuGlyTyr 21
|||||
Db 16 CTCTTCTCGGACCTTCACTCGCTTCA-----ATTGCGAAAGCATATACGGCGT 66
QY 22 PrometasPThrGlySerHisProIleGluAlaValAspProGluValLysThrGluVal 41
|||||
Db 67 GCTTTG-----AGCGAGCGTCTCGCAATATATATGACGAAACCCCGACGAAAG 120

QY 42 PheAlaAspSerLeuLeuAlaAlaAlaGlyAspAsp----- 53
|||||
Db 121 GCTGCC-----CTGGACGCCATCGTGAAGATGACCTGCCATGTTTCAGAAATCTG 174
QY 54 ---AspTrpGluSerProProTyrAsnLeuLeuTyrArgAsnAlaLeuProIleProPro 72
|||||
Db 175 AAGAGCTGGCAAAACCCCGAGTATCCATCTCTTTTGGCGAGGACAGTCCCATTCCTCA 234
QY 73 VallysGlnProLys 77
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Db 235 GCCAAGAGAACCGAAGTATGAGTCTGAATTCATGACAGAGTTCCTAGAAATGCTCA 294
QY 78 -----MetIleThrAsnProValThrGlyLysAspIleTrrpTyrGluIle 94
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Db 295 CCCATCCGCAAGTAAATGACGAATCTGTCCAAACAGAGATCTGTGACTACAGAAAT 354
QY 95 GluIleLysProPheGlnArgIleTyrProThrLeuArgProAlaThrLeuValGly 114
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Db 355 GTATCAAAACCTTTAACCAACAGGTCTATCCAAAGTCTAGTCTCGCTGGTGGTGGC 414
QY 115 TyrAspGlyMetSerProGlyProThrPheAsnValProArgGlyThrGluValVal 134
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Db 415 TATGATGCAATTCACACAGGCCCTACATCATCTGCCGAGAGAGAACAGAGCCGTTGTA 474
QY 135 ArgPheIleAsnAsnAlaThrValGluAsnSerValHisLeuHisGlySerProSerArg 154
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Db 475 CGATTGTAACCAAGGCTGATCGGAAAGTTCATTCATCTCATGTTCTCCCTCCGT 534
QY 155 AlaProPheAspGlyTrrpAlaGluAspValThrPheProGly----- 168
|||||
Db 535 GCCCCTTTACGAGTGGCTGAAGATTGAT-TATGAAGGCCAATTCAAGGTACAC 593
QY 169 -----GluTyrLysAspTyr 173
|||||
Db 594 AGAACAATCTATGATCATCAGGCTGCTCTTTATACACAGCATGCTTCTTACACTAC 653
QY 174 TyrPheProAsnTyrGlnSerAlaArgLeuLeuTrrpTyrHisAspHisAla----- 190
|||||
Db 654 TACTACCGCAACCAACAGGCTGCGATTCCTGTGGTACACAGTATGCTATGATCATGTT 713
QY 191 -----PheMetLys 193
|||||
Db 714 GTAAGTCTTCAGACTATCATGAGGAGCAAGCAAGCAATCGGCTGACACTTATTCAG 773
QY 194 ThrAlaGluAsnAlaTyrPheGlyGlnAlaGlyAlaTyrIleIleAsnAspGluAlaGlu 213
|||||
Db 774 ACTCGGGAATAATGCTATTTTGGACAGGCTGGCCCTACCTGATCACAGACACCAAGCTGAG 833
QY 214 AspAlaLeuGlyLeuProSerglyTyrGlyGlnPheAspIleProLeuIleLeuThrAla 233
|||||
Db 834 GAGCCCTCGGCTCTCTTGGGTATGAGAAATACACATCCACTGGGTGCTAGTTC 893
QY 234 LysTyrTyrAsnAlaAspGlyThrLeuArgSerThrGluGlyLysAspGlnAspLeuTrrp 253
|||||
Db 894 AAGTTCACAAACAGTATGATGACCTCTCCAGACAGTGGAGAGAAACAGAGCTCTGG 953
QY 254 GlyAspValIleHisValAsnGlyGlnProTrrpProPheLeuAsnValGlnProArgLys 273
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Db 954 GCGGACGTCAATCCATGCAACAGGCTGACCCCTGCGCATCTTCAACGTTGAGCCCTGCAAG 1013
QY 274 TyrArgPheArgPheLeuAsnAlaAlaValSerArgAlaTrrpLeuLeuTyrLeuValArg 293
|||||
Db 1014 TATGCTCTGATTCCTCAATGCGGCTGTTTCTGGAATCTTGCCTCTATTTCTGACAG 1073
QY 294 ThrSerSerProAsnValArgIleProPheGlnValIleAlaSerAspAlaGlyLeuLeu 313
|||||
Db 1074 CAACAAGCCACGTGCTATACACTTCTTCCAGGTCTTCCTCTGTATGAGAGGCTACTC 1133
QY 314 GlnAlaProValGlnThrSerAsnLeuTyrLeuAlaValAlaGluArgTyrGluIleIle 333
|||||
Db 1134 ACCGACCCGCTCCAAACCTCAGATATTTAGCTGGACAGACAGAGCGCTACGAGATTGTA 1193

QY 334 IleAspPheThrAsnPheAlaGlyIleThrLeuAspLeuArgAsnValAlaGlyIleThrAsn 353
Db 1194 TTCGACTTTCGCCCTTATGACAGCCAGATAGATTTTCCCTTAACCTTGCACAAAGGCCAAT 1253
QY 354 AspValGlyAspGluAspGluThrAlaArgThrLeuGluValMetArgPheValSer 373
Db 1254 GGGGTCCGACCGATGACGATTTATCCAAACACTGCACAAAGTATCGGCTTCATCTCAAC 1313
QY 374 SerGlyThrValGluAspAsnSerGlnValProSerThrLeuArgAspValProPhePro 393
Db 1314 AGCCAAGACGTGCTGATACCTGGGTGACCCGACAGCTATCTCCAGATCCAGTTCCCC 1373
QY 394 ProHisGlyGluGlyProAlaAspGlyHisPheGlyPheGluArgSerAsnGlyHisTyr 413
Db 1374 GCCGCAAAACCCGGC---ATCGACCCACCACTTCCCTTCATCCGACCAACAGCAGTGG 1430
QY 414 LeuIleAsnAspValGlyPheAlaAspValAsnGluArgValLeuAlaGlySerProGluLeu 433
Db 1431 CGCATCAACGGCATGGGTTTCCACAGCTCCAGAACCGTATCTGCGCCAGATCCGCCGC 1490
QY 434 GlyThrValGluValTyrGluLeuGluAsnSerSerGlyGlyTyrPheHisProValHis 453
Db 1491 GGCACCTGTCGAGCTATGGAACCTGAGAACAGCTCCGGGGCTGTGCGACCCCATTCAC 1550
QY 454 IleHisLeuValAspPheGlyHisLeuGlyArgThrGlyGly-----ArgGlyGln 470
Db 1551 GCCACCTGTCGAGCTTCCGAGTCTCCGACCGCTGACGAAAGCAGTCCGCCGC--- 1607
QY 471 ValMetProGlyGluSerAlaGlyLeuGlyAspValValTyrPheGlyArgGlyGlyLeu 490
Db 1608 GTCAATGCCCTACGATCCGCCGCTCTCAAGAGCTGCTGTGCTGCGCCGACACAGAG 1667
QY 491 LeuThrIleGluAlaHisTyrGlnProThrPheGlyAlaTyrMetThrPheHisAsn 510
Db 1668 GTGCTGTCGAGGACACTACGCCCCCTGGGACGAGTACATGATGTCACATGCCACAAAC 1727
QY 511 LeuIleHisGluAspAsnAspMetMetAlaValPheAsnValThrAlaMetGluLeuGly 530
Db 1728 CTGATCCAGAACCAACATGATGAGCCGCTTTCAGTCACTCACTCCAGAACCTTT 1787
QY 531 GlyTyrLeuGln---GluAspPheGluAspProMetAsnProLysTyrArgAlaValPro 549
Db 1788 GGGTCAACAGACAGACGATTTCCACGACCCGGAAGATTCGCTGGTGTCCAGAACCC 1847
QY 550 TyrAsnArgAsnAspPheHisAlaArgAlaGlyAsnPheSerAlaGlySerIleThrAla 569
Db 1848 TTCACCGCGGCTGATGACGCGGATCGGCTATCTTCAGAGCATCCATCAGGCT 1907
QY 570 ArgValGlnGluLeuAlaGluGluProTyrAsnArgLeuAspGluIleLeuGluAsp 589
Db 1908 AGAGTGAACGAGTTGGCGCTGGACAGCCGTCACAGCACTGACAGGTCACGGCTCG 1967
QY 590 Leu 590
Db 1968 CTC 1970

RESULT 5
AR211555 2905 bp DNA linear PAT 20-JUN-2002
LOCUS AR211555
DEFINITION Sequence 3 from patent US 6399329.
ACCESSION AR211555
VERSION AR211555.1 GI:21514907
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE Unclassified.
1 (bases 1 to 2905)
AUTHORS Wang, H. and Bodie, E. A.
TITLE Phenol oxidizing enzymes
JOURNAL Patent: US 6399329-A 3 04-JUN-2002;
FEATURES Location/Qualifiers
1..2905
/organism="unknown"

BASE COUNT 714 a 792 c 664 g 734 t 1 others
ORIGIN
Alignment Scores:
Pred. No.: 5,55e-141
Score: 1868.00 Matches: 2905
Percent Similarity: 67.82% Conservative: 81
Best Local Similarity: 55.59% Mismatches: 132
Query Match: 58.58% Indels: 83
DB: 6 Gaps: 10
US-10-080-233-2 (1-594) x AR211555 (1-2905)
QY 2 LeuPheLysSerTyrPheGluLeuAlaAlaAlaSerGlyLeuLeuSerGlyValLeuGlyIle 21
Db 129 CTCTTCGACGACTTCACACTCGTTCA-----ATTGGGAAGGATATACGGYGTG 179
QY 22 ProMetAspThrGlySerHisProIleGluAlaValAspProGluValLysThrGlyVal 41
Db 180 GCTTTG-----AGCGAAGCTCCCGCAAAATTTGTGCACAAACCCCGACGAAGAAAAG 233
QY 42 PheAlaAspSerLeuLeuAlaAlaAlaGlyAspAsp----- 53
Db 234 GCTGCC-----TTGGCTCAATTGTGAAGATGACCTCGCGGATGTTCACATGCTG 287
QY 54 ---AspTyrPheGluSerProTyrAsnLeuLeuTyrArgAsnAlaLeuProIleProPro 72
Db 288 AAAGACTGGCAAAAGCCGAGATATCTCATTTTTCGCCAACCACATCCCATCCATCCCA 347
QY 73 ValLysGlnProLysMetIle----- 79
Db 348 GCCAAGAACCAAAAGTA-GTAGTGTTCATTCGATCGACAGGTTTCTTAAGATATATCTC 406
QY 80 -----IleThrAsnProValThrGlyLysAspIleTyrTyrGlyIle 94
Db 407 ACCATCCACAGTAAACTACGATTCCTCCAAACAAAGAGATATGTTACTAGAGATT 466
QY 95 GluIleLysProPheGlnAlaArgIleTyrProThrLeuArgProAlaThrLeuValGly 114
Db 467 GTCATCAAAACCTTCAACCACAGAGTATATCAAGACCTCGCCCTGTTAGTAGGC 526
QY 115 TyrAspGlyMetSerProGlyProThrPheAsnValProArgGlyThrValVal 134
Db 527 TATGACGGCATCTCCCGAGTCTCAATGATAGCGGAGAGAAAGAAAGCTGTGTGA 586
QY 135 ArgPheIleAsnAsnAlaThrValGluAsnSerValHisLeuHisGlySerProSerArg 154
Db 587 CGGTTTATAAACAGGGTATCGGGAAGCTCCATCTCCACGGCTCCCGCTCCCGCT 646
QY 155 AlaProPheAspGlyTyrAlaGluAspValThrPheProGlyGlyTyrLys----- 171
Db 647 GCCCCTTTTGACGAGTGGGTGATGATGATCAATGAAGGGGGAATACAA-AGGTACGAT 705
QY 172 -----Asp 172
Db 706 AGCGTGTATCTACGCAATCAGAAAGCCTTATCATCTAACAAGACTTTTCTTCACAG 765
QY 173 TyrTyrPheProAsnTyrGlnSerAlaArgLeuLeuTyrTyrHisAspHisAlaPhe-Me 192
Db 766 TACTACTACCGCAACCAACCAAGCTGCCGATTTTGTGGTACACGATCATGCTATGAT 825
QY 192 t----- 192
Db 826 GTTGAAGTCTTTACCGACTTTTCATGTTAGTGAACGGAAGATTAAGTAAACATCTGT 885
QY 193 -LysThrAlaGluAsnAlaTyrPheGlyGlnAlaGlyAlaTyrIleIleAsnAspGluAl 212
Db 886 GCAGACCGCAGAAAATGCTATTTCCGGCAAGCCGGGCTTACCTGATCAGACACCGCG 945
QY aglAspAlaLeuGlyLeuProSerGlyTyrGlyGluPheAspIleProLeuIleLeuTh 232
Db 946 TGAGGATGCTCTCGGCTTCTTCAAGGTTACGGAAATATACACATTCGCTGCTCTCAG 1005

[illegible]

Db	2083	GCFC	2086	111
RESULT 6				
MYRBOR				
LOCUS			1942 bp	mRNA
DEFINITION				linear
ACCESSION				PLN 01-FEB-2000
VERSION				
KEYWORDS				
SOURCE				
ORGANISM				
REFERENCE				
AUTHORS				
TITLE				
JOURNAL				
MEDLINE				
REFERENCE				
AUTHORS				
TITLE				
JOURNAL				
COMMENT				
FEATURES				
source				
CDS				
sig_peptide				
mat_peptide				
polya_signal				
polya_site				
BASE COUNT	440 a	549 c	436 g	517 t
ORIGIN				
Alignment Scores:				
Pred. NO.:	1.22e-129		Length:	1942
Score:	1724.50		Matches:	322
Percent Similarity:	74.34%		Conservative:	75
Best Local Similarity:	60.30%		Mismatches:	128
Query Match:	54.08%		Indels:	9

DB: 8 Gaps: 7

US-10-080-233-2 (1-594) x MYRBOR (1-1942)

QY	57	SerProProtyrAsnLeuLeuTyrrgrAsnAlaLeuProIleProProValIysGlnPro	76
Db	192	AGCCACAGATATCCC---ATGTCACAGTACACATGCCAATTCCTCGTTAAAGACGCC	248
QY	77	LysMetIleIleThrAsnProValThrIlyAspIleTrrPtyrGluIleGluIle	96
Db	249	CGCTTGACTGTAACCAATCTGTGTAAATGAGCAAGAGATCTGTACTATGAGGTCCAGATC	308
QY	97	LysProPheGlnGlnArgIleTyrrProThrLeuArgProAlaThrLeuValGlyTyrrAsp	116
Db	309	AAGCCCTTCACTACACACAGGTTTACCCTTACCTTGGATCCGCTGATCTGTGGGATATAT	368
QY	117	GlyMetSerProGlyProThrPheAsnValProArgIlyThrGluThrValValArgPhe	136
Db	369	GGATATGTCCTCGGCCCTACTTCCAGGTCTCTCGTGAGTGTGAACAAGTTGTCCGCTTC	428
QY	137	IleAsnAsnAlaThrValGluAsnSerValHisLeuHisGlySerProSerArgAlaPro	156
Db	429	ATTAAACAATGCTGAGGCTCTTAACCTCCCTTACCCTGACGCGATCTTCTCTCGTCCGCC	488
QY	157	PheAspGlyTrrPAlaGluAspValThrPheProGlyGluTyrrLysAspTyrrTyrrPhePro	176
Db	489	TTTGACGGATGGCGAGAGACATCCAGCCTGGCAGCTTCAAAAGACTATATTAACCA	548
QY	177	AsnTyrrGlnSerAlaArgLeuLeuTrrPyrHisAspHisAlaPheMetLysThrAlaGlu	196
Db	549	AATGACAGCTGCTGCTGATACCTTAATGTAACACAGATCATGTAATCATACATCCTGAG	608
QY	197	AsnAlaTyrrPheGlyGlnAlaGlyAlaTyrrIleIleAsnAspGluAlaGluAspAlaLeu	216
Db	609	AACCCCTAACCTGGCCAGCTGGTCTCAATGCTCACTGACCAAGCCGAAGACCTCTTC	668
QY	217	GlyLeuProSerGlyTyrrGlyGluPheAspIleProLeuIleLeuThrAlaLysTyrr	236
Db	669	AACCTTGCCAACTGGATATGGAGGTTCGATATTCCAAATGATCTTCACTCCAAAGCAATAT	728
QY	237	AsnAlaAspGlyThrLeuArgSerThrGluGluAspGlnAspLeuTrrPglYAspVal	256
Db	729	ACGGCAAAAGCGCAACTTGGTCACACACTATATGGAAGCGTAACATCTTGTGGGTATGTA	788
QY	257	IleHisValAsnGlyGlnProTrrProPheLeuAsnValGlnProArgLysTyrrArgPhe	276
Db	789	ATTACAGCGAAGCGTCAACCTTGGCTTCAAGAACGTTGAGCCCTCGCAAAATATGATTC	848
QY	277	ArgPheLeuAsnAlaValSerArgAlaThrLeuLeuTyrrLeuValArgThrSerSer	296
Db	849	CGCTTCCTCGATGCGCGGAGTTCGTGCTTTCGGCTTTCATCTTGGTGCATATCATATCT	908
QY	297	ProAsnValArgIleProPheGlnValIleAlaSerAspAlaGlyLeuLeuGlnAlaPro	316
Db	909	ATGCAACACTGCTTGCCTTTCAGGTATATTCCTCCGATTTCTGGCTTCTTGAACACCTT	968
QY	317	ValGlnThrSerAsnLeuTyrrLeuAlaValAlaGluArgTyrrGluIleIleAspPhe	336
Db	969	GCCGATATCACAGCTTGTGATCATTTCCATGCGCCAGCGTACGAAGTGTGTGGACTTC	1028
QY	337	ThrAsnPheAlaGlyGlnThrLeuAspLeuArgAsnVal---AlaGluThrAsnAspVal	355
Db	1029	TCCGACTATGTGTCGCAAGACTATTTGAACTTCGCGAACTGGGCGGTAGCATTTGGCGGACTC	1088
QY	356	GlyAspGluAspGlyTyrrValArgThrLeuGluValMetArgPheValValSerSerGly	375
Db	1089	GGAAACACATCCGAGCTATGACAACAACGACAAAGTCAATGCTTTCGTGTACGACACAC	1148
QY	376	ThrValGlu---AspAsnSerGlnValProSerThrLeuArgAspValProPhePro---	393
Db	1149	ACAACCTGACGAGATACCTCAGTTGTCTCTGCTCAACCTTGCTGATGTTCCTTCCCTCT	1208
QY	394	ProHisLysGluGlyProAlaAspLysHisPheLysPheGluArgSerAsnGlyHisTyrr	413

[illegible]

BASE COUNT 457 a 549 c 436 g 517 t
 ORIGIN

Alignment Scores:
 Pred. No.: 1.23e-129 Length: 1959
 Score: 1724.50 Matches: 322
 Percent Similarity: 74.34% Conservative: 75
 Best Local Similarity: 60.30% Mismatches: 128
 Query Match: 54.08% Indels: 9
 Gaps: 7

US-10-080-233-2 (1-594) x E05283 (1-1959)

QY 57 SerProProTyrAsnLeuLeuTyrArgAsnAlaLeuProIleProProValLysGlnPro 76
 DB 132 ACCCCACAGTATCCC---ATGTTCACAGTACACACATCCCAATTCCTCTGTAAGCAGCC 248

QY 77 LysMetIleIleThrAsnProValThrGlyLysAspIleTyrTyrGluIleGluIle 96
 DB 249 CGCTTGACGTACCAACATCTCTGATGACAGAGATGCTGCTACTATGAGTCCAGATC 308

QY 97 LysProIleGlnIleArgIleTyrProThrLeuArgProAlaThrLeuValGlyTyrAsp 116
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QY 117 GlyMetSerProGlyProThrPheAsnValProArgGlyThrGluThrValAlaArgPhe 136
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QY 137 IleAsnAsnAlaThrValGluAsnSerValIleLeuHisGlySerProSerArgAlaPro 156
 DB 429 ATTACAAATGCTGAGGCTCTTAACATCCGTTACCTGCACAGGATTCCTCGTGGCCGC 488

QY 157 PheAspGlyTyrAlaGluAspValThrPheProGlyTyrLysAspTyrTyrPhePro 176
 DB 489 TTGACGATGGGAGAGACATCACCGACCTGCAGCTCAAGACATTAATTAACCA 548

QY 177 AsnTyrGlnSerAlaArgLeuLeuTyrTyrHisAspHisAlaPheMetLysThrAlaGlu 196
 DB 549 AATACACAGTCTGCTCGTACCTATGCTACACAGATCATGCTATGCTACTGCTGAG 608

QY 197 AsnAlaTyrPheGlyGlnAlaGlyAlaTyrIleIleAsnAspGluAlaGluAspAlaLeu 216
 DB 609 AACGCTACCGTGGGAGGCTGCTCTCATGCTACACTGACCGACGACGACGCTGTC 668

QY 217 GlyLeuProSerGlyTyrGlyGluPheAspIleProLeuIleLeuThrAlaLysTyrTyr 236
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QY 237 AsnAlaAspGlyThrLeuArgSerThrGluGluAspGlnAspLeuTyrPglLysAspVal 256
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 DB 789 ATTCACGTAACGCGCAACCTGCGCTTCAAGAGCTGACCTCGCAATATGATGATTC 848

QY 277 ArgPheLeuAsnAlaValSerArgAlaThrPheLeuTyrLeuValAlaArgThrSerSer 296
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QY 297 ProAsnValArgIleProPheGlnValIleAlaSerAspAlaGlyLeuLeuGlnAlaPro 316
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QY 317 ValGlnThrSerAsnLeuTyrLeuAlaValAlaGluArgTyrGluIleIleIleAspPhe 336
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 DB 1149 ACACACTACACAGATATCCTGAGTTCCTGTAACCTTCGATGATCTCCCTCCCTCT 1208

QY 394 ProHisLysGluGlyProAlaAspLysHisPheLysPheGluArgSerAsnGlyHisTyr 413
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QY 414 LeuIleAsnAspValGlyPheAlaAspValAsnGluArgValLeuAlaLysProGluLeu 433
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QY 572 GlnGluLeuAlaGluGlnLupProTyrAsnArgLeuAspGlu 585
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RESULT 8
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 DEFINITION Acromonium murorum mRNA for polyphenol oxidase (pPOA gene).
 ACCESSION AJ271104
 VERSION AJ271104.1 GI:6996277
 KEYWORDS oxidase; pPOA gene.
 SOURCE Acromonium murorum.
 ORGANISM Acromonium murorum
 Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
 Hypocreales; Hypocreaceae; mitosporic Hypocreaceae; Acromonium.
 REFERENCE 1 (bases 1 to 2126)
 AUTHORS Gouka,R.J., van der Heiden,M., Swarthoff,T. and Verrips,C.T.
 TITLE Cloning of a phenol oxidase gene from Acromonium murorum and its
 JOURNAL expression in Aspergillus awamori
 MEDLINE Appl. Environ. Microbiol. 67 (6), 2610-2616 (2001)
 PUBMED 11375170
 21268855
 2 (bases 1 to 2126)
 REFERENCE Gouka,R.J.
 AUTHORS Submitted (19-JAN-2000) Gouka R.J., Biotechnology, Unilever
 TITLE Research Vlaardingen, Olivier van Noortlaan 120, 3133 AT
 JOURNAL Vlaardingen, NETHERLANDS
 FEATURES Location/Qualifiers

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5' UTR	15. .97 /gene="ppoa" /product="polyphenol oxidase"
CDS	98. .1906 /gene="ppoa" /codon_start=1 /product="polyphenol oxidase" /protein_id="CAB75422.1" /db_xref="GI:6996278" /db_xref="SPTREMBL:Q9P8C3" /translation="MAATLALALALYLISKGAQAMKFEIIPDEBAALAAIVEDD PANDLQSPANDLQKRSPLSPATLQAPLSIPVPEPLTVNPNYNGSIDYEIE IKHSEQVPEPLQSPADLVGDIISPGPTFIDKGRSEVRFVNAKATYESSJHLGSES RAPDGAEDVTNPGEKKDYIYPNAGRGRESEFEDHAMHETAEANVGOAGGYIHP AEDSLGDSGGEYDIPILITSKQYNDSGTFESKGETOSLMDVLOVNGVPMYEPV EPRKRRRLDAVSRSESLFTVDTADERTIPQVYASDSGLLEEVYTSKVLSTA ERYELIDSDSEKRTIELRNEPAAVGGILEVNVDDVDKVRFNVAAGPLSSPOTSVV PSTLRDVPSPSTTIDHSFRPARGOMSVINFTSDVENRLIANVPLGTYLOMDL TNAAGQTHPIHILVDPEKILSRTGAATGATTREVEYESAGLKDYVILGKGTVEVE AHVAPGWYPIHCHLHEDNDMAAFENVYLDVGNSTALADPMQDERAKPYVD NDVEYRENAFTSDLEIAVQVMAVLYLFDNDMEIV" 98. .160 /gene="ppoa" 281. .1903 /gene="ppoa" /product="polyphenol oxidase" /evidence="experimental" 161. .280 /gene="ppoa" /note="polyphenol oxidase propeptide" 1907. .2120 /gene="ppoa" 2073 polyA_site BASE COUNT 442 a 723 c 546 g 415 t ORIGIN
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3' UTR	1907. .2120 /gene="ppoa" 2073
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Matches:	328
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OS-10-080-233-2 (1-594) x AMU2711104 (1-2126)	
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290 AGCCGCGGGTACAGG--CTGTTCCAGGCGCGCGCTGTGCATCCCTCCGTCAGAGACCT 346	: : : : : : : :
77 LysMetIleIleTrpAsnProValThcGlyLysAspIleTyrTyrGluIleGluIle 96	::: : : : : : : :
347 CTCCTTCACCGACACACCCCTACACAGCGTGGGAGATCGACTGATGAGATCGAATC 406	::: : : : : : : :
97 LysProPheGlnGlnArgIleTyrProThrLeuArgProAlaThrLeuValGlyTyrAsp 116	: : : : :
407 AAGCACTTCTGTGACAGGCTTTCCTGACCTGGGCGCTGTGACCTGTGGCTACGAC 466	: : : : :
117 GlyMetSerProGlyProThrPheAsnValProArgGlyThrGluThrValValArgPhe 136	
467 GGCATCTGCGCCGCTCTTATTCACGAGAAAGGACGAGACGCTGCTCCGCTTC 526	
137 IleAsnAsnAlaThrValGluAsnSerValHisLeuHisGlySerProSerArgAlaPro 156	

Dd		1604	GAGACGGTCTGTCGACAGGCCTCACTAGCCTCTTGCGCCGCCGTGTACTATTTCCACATGC	1663
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Dd		1664	CACAACCCTCATCCACAGAGCACACGACATGATGGCCGCCCTCAACAGTCCACGGTCTCCCC	1723
Oy		529	GlulysgLyTYrLeugIngluAsPhegluAsPProMetAnPrOlySTfRAtgAlAval	548
Dd		1724	GACTACGGCTVCAACACTCGACGGCCCTCGCTTACCCCACAAAGCAGAACGACTTCGGGCCAAG	1783
Oy		549	ProTyraSnArAgAsnAspPheHisalAarglaLghAsnPheSerAlagluSeRIethr	568
Dd		1784	CCGTACGTGGAGCAACAGCGTGCAGAGTGGCGGAGAACGCCCTTCAGCACCAGCAAGATCGAG	1843
Oy		569	AlaarYalngluLeualaglIngluProTyraSnArAgLeuAsp--GlulIedu	587
Dd		1844	GCGCAGGCHCAGCTGATGCGCAGCTACCTGCCCTACGACACCCGAGACTGGAGATGCTC	1903
		588	GIuAspleuglylleglu 593	
		1904	TAAAGTGTGCTGACTGGAC 1921	
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DEFINITION	Sequence 1 from patent US 6168936.			
ACCESSION	ARI122996			
VERSION	ARI122996.1		GI:14107962	
KEYWORDS	.			
SOURCE	Unknown.			
ORGANISM	Unclassified.			
REFERENCE	1 (bases 1 to 1958)			
AUTHORS	Wang, H.			
TITLE	Phenol oxidizing enzymes			
JOURNAL	Patent: us 6168936-A 1 02-JAN-2001;			
FEATURES	Location/Qualifiers			
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Score:	1620.50	Matches:	331	
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OS-10-080-233-2 (1-594) x ARI122996 (1-1958)				
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Oy		77	Lys-----Met-Ile11 80	
Dd		202	AAGAATAAGTAACATTCTATAGCGCTAGACAGACCAAGCTTGCATATCATTCAGTACCGCT	261
Oy		80	eThAsnProValThrGlyLysAspIleTFtyTYrgluIlegluilelSproPhegl	100
Dd		262	CCCCAACCCCAACACTGTGAGAGGACACCTTGTACTACGAGATGAGATTAGGCCCTTCTC	321
Oy		100	nGlnArgIleLeuTyProThrIleuAvgrProAlaThrLeuValGlyTyraSpJymetSer	120
Dd		322	CCACCAAGATCTACCGCTGATCTGGAGCGCGCCACACATGGTGGATACGATGGCATGTCCCC	381
Oy		120	oGlyProThrPheAsnValProArGlyThrGluThrValValArGrPheIleAsnAl	140
Dd		382	AGGACCTACCATCATCCTGCTCGTGGACATGGAAGTGTGTCTGCCCTTCGTAACAGCGG	441
Oy		140	a-----ThyValGIuAsnSerValHIsleuHISGLYSerProSerAlgrAlaProPheAs	158

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GenCore version 5.1.6
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OM protein - nucleic search, using frame_plus_p2n model

Run on: July 3, 2003, 20:55:31 ; Search time 381 seconds

(without alignments)
3510.990 Million cell updates/sec

Title: US-10-080-233-2

Perfect score: 3189

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Scoring table:

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Delop 6.0, Delext 7.0

Searched: 2185239 seqs, 1125999159 residues

Total number of hits satisfying chosen parameters: 4370478

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Post-processing: Minimum Match 08
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Listing first 45 summaries

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Prod. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	3189	100.0	1791	20	AA227601	Stachybotrys pheno
2	3189	100.0	1791	21	AA50019	Stachybotrys chart
3	3189	100.0	1791	21	AA51314	Stachybotrys chart
4	3189	100.0	1791	24	AA47584	S. chartarum phenol
5	3171	99.4	1791	20	AA25727	Stachybotrys chart
6	3056	95.8	1791	20	AA22535	Stachybotrys chart
7	3056	95.8	1791	20	AA227608	Stachybotrys pheno
8	3056	95.8	1791	20	AA225728	Stachybotrys pheno
9	3056	95.8	1791	20	AA227602	Stachybotrys pheno
10	3056	95.8	1791	21	AA50018	Stachybotrys chart
11	3056	95.8	1791	21	AA51313	Stachybotrys chart
12	3056	95.8	1791	24	AA47582	S. chartarum phenol
13	3056	95.8	1791	24	AA47582	S. chartarum phenol
14	1870	58.6	2063	21	AA50021	Curvularia pallasc
15	1870	58.6	2063	21	AA51316	Curvularia pallasc
16	1870	58.6	2063	24	AA47585	C. pallascens pheno
17	1868	58.6	2905	21	AA50020	Bipolaris spicifer
18	1868	58.6	2905	21	AA51315	Bipolaris spicifer
19	1868	58.6	2905	24	AA47583	B. spicifera phenol
20	1724.5	54.1	1959	14	AA047790	Bilirubin oxidase
21	1708.5	53.6	2110	21	AA621243	DNA encoding a phe
22	1620.5	50.8	1958	21	AA682585	Stachybotrys chart
23	1620.5	50.8	1958	22	AA630028	Stachybotrys chart
24	1620.5	50.8	1958	24	ABK50918	DNA encoding pheno
25	1620.5	50.8	1958	24	ABK53881	Stachybotrys chart
26	1620.5	50.8	1958	22	AA682586	Stachybotrys chart
27	1620.5	50.8	1958	22	AA630029	Stachybotrys chart
28	1620.5	50.8	1958	24	ABK50919	Stachybotrys chart
29	1620.5	50.8	1958	24	ABK53882	Stachybotrys chart
30	694.5	21.8	1470	24	ABK74913	Bacillus licheniflo
31	666.5	20.9	858	21	AA50022	Americosporium atrum
32	666.5	20.9	858	21	AA51317	Americosporium atrum
33	666.5	20.9	858	24	AA47586	A. atrum phenol oxi
34	588	18.4	109319	22	AA508693	Micromonospora DNA
35	516.5	16.2	3446	23	ABU5057	Micromonospora car
36	500	15.7	1533	22	AAH66018	C. glutamicum codin
37	500	15.7	1533	22	AAH66018	C. glutamicum codin
38	500	15.7	1533	22	AAH66018	C. glutamicum codin
39	480.5	15.1	1434	22	AAH53928	S. epidermidis ope
40	472	14.8	2014	21	AAH47954	Arabidopsis thalia
41	409.5	12.8	969	24	ABN90646	Staphylococcus epi
42	365.5	11.5	3800	22	AAH54957	S. epidermidis gen
43	363.5	11.4	1230	22	AAH53932	S. epidermidis ope
44	363.5	11.4	1230	22	AAH54003	S. epidermidis gen
45	354.5	11.1	3410	22	AAH54141	S. epidermidis gen

ALIGNMENTS

RESULT 1
AA227601
ID AA227601 standard; DNA; 1791 BP.

AC AA227601;
XX 16-DEC-1999 (first entry)

DE Stachybotrys phenol oxidase coding sequence.

KW Phenol oxidase; enzyme; coloured compound; dye transfer prevention;

KW fabric washing; stain bleaching; anti-dye transfer; detergent; ss.

XX Stachybotrys chartarum.

OS W09949020-A2.

XX 30-SEP-1999.


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Oy 361 TyrAlaArgThrLeuGluValMetArgPheValValSerSerGlyThrValG|YAspAsn 380
Db 1087 TACGCTGCACCTCTCGAGGTATGCGCTTCGTCGACCTCTGCGACCTGTTGAGACAC 1146
Oy 381 SerGluValProSerThrLeuArgAspValProPheProOHHisLysGluGlyProAla 400
Db 1147 AGCCAGGTCCCTCCACTCTCCGTACCTCTTCTCCCTCCACAAAGAGGCCCCGCC 1206
Oy 401 AspLysHisPheLysPheGluArgSerAsnGlyHisLysLysLeuLeuAspValG|YIhe 420
Db 1207 GACAAGCACTTCAAGTTGAAGGACGACAGCAAGACACTACCTGATCAACGATGTGGCTTT 1266
Oy 421 AlaAspValAsnGluArgValLeuAlaLysProGluLeuGlyThrValG|YValTPS1u 440
Db 1267 GCCGATGTCATGAGCGCTGCTGGCCAAAGCCCGACGCTCGGACCGTTGAGGTCTGGAG 1326
Oy 441 LeuGluAsnSerSerGlyGlyTrpSerHisProValHisLysLeuValAspPheLys 460
Db 1327 CTCGAGAACTCTCTGGAGGCTGGAGCCACCCCGCTCCACATTCACCTTGTGACTTCAAG 1386
Oy 461 IleLeuLysArgThrGlyGlyArgGlyGluValMetProGlyLysSerAlaGlyLeuLys 480
Db 1387 ATCTCAAGCAAGCACTGGTGTGCTGGCCAGGTCATGCTCGAGTCTGCTGTCTTAAG 1446
Oy 481 AspValValTrpLeuGlyArgGlyGluThrLeuThrIleGluAlaHisLysTrpGluProTrp 500
Db 1447 GATCTCGTCTGTTGGGCGAGGGGTGAGACCTTGACCATGAGAGGCCACTTACCAACCTTGG 1506
Oy 501 ThrGlyAlaTrpMetTrpHisCysHisAsnLeuIleHisGluAspAsnAspMetMetAla 520
Db 1507 ACTGAGCTTACATGTGCTGCTGCTACCAACTCATCTCAAGAGATTAACGACATGATGCT 1566
Oy 521 ValPheAsnValTrpAlaMetGluGluLysGlyTrpLeuGluGluAspPheGluAspPro 540
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Oy 541 MetAsnProLysTrpArgAlaValProTrpAsnArgAsnAspPheHisAlaArgAlaGly 560
Db 1627 ATGAACCCCAAGTGGCGCGCTTCTTACAAACGCAACGACTTCCATGCTCGCGCTTGA 1686
Oy 561 AsnPheSerAlaGluSerIleThrAlaArgValGluGluAlaGluGluProTrp 580
Db 1687 AACTTCTCCCGGAGTCCATCTACTGCGGAGTGGCGAGCTGGCCGAGCAGAGCCGTAC 1746
Oy 581 AsnArgLeuAspGluIleLeuGluAspLeuGlyIleGluGlu 594
Db 1747 AACCGCCTCGATGAGATCTCGAGAGATCTTGAATCGAGGAG 1788

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RESULT 3
AA51314 standard; DNA; 1791 BP.

AA51314:
09-OCT-2000 (first entry)
Stachybotrys chartarum phenol oxidizing enzyme cDNA.
Phenol oxidizing enzyme; colour; dye; modification; detergent; stain;
pulp; paper bleaching; ss.
Stachybotrys chartarum.
Key location/Qualifiers
CDS 7..1791
FT /*tag= a

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FT  /product= Phenol_Oxidizing_Enzyme
PN  MO200037654-A2.
XX  29-JUN-2000.
PD  20-DEC-1999; 99WO-US31009.
XX  23-DEC-1998; 98US-0220871.
PR  23-JUN-1999; 99US-0338723.
XX  (GENV ) GENENCOR INT INC.
PA  Wang H, Bodle EA.
PI  WPI: 2000-452191/39.
DR  P-PSDB; AA196761.
XX  New phenol oxidizing enzyme for modifying colors associated with dyes
XX  or colored compounds, is obtained from fungus and is encoded by a
XX  nucleic acid comprising a specific nucleotide sequence
XX  Disclousre: Fig 5A-B; 45pp; English.
PS  This cDNA encodes Stachybotrys chartarum phenol oxidizing enzyme.
CC  Phenol oxidizing enzymes encoded by nucleic acid sequences which
CC  hybridize to this DNA are claimed, as long as the enzyme is capable of
CC  modifying the colour associated with dyes or coloured compounds. The
CC  enzymes are useful in detergent compositions and for modifying colors
CC  associated with dyes or colored compounds which occur in stains in a
CC  sample. The enzymes are also useful for pulp and paper bleaching,
CC  anti-dye transfer in detergent and other textile applications.
SQ  Sequence 1791 BP; 380 A; 551 C; 451 G; 409 T; 0 other;

Alignment Scores:
Pred. No.: 3.68e-303 Length: 1791
Score: 3189.00 Matches: 594
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 21 gaps: 0

US-10-080-233-2 (1-594) x AA51314 (1-1791)
Oy 1 MetLeuPheLysSerTrpGluLeuAlaAlaLaserglyLeuSerGlyValLeuGly 20
Db 7 ATGCTGTTCAGTCAATGCGCACTGGACACCTCCGGCTCCTGTGAGTCTCTGGC 66
Oy 21 IleProMetAspThrGlySerHisProIleGluAlaValAspProGluValLysThrGlu 40
Db 67 ATCCGATGACACCGCGAGCCACCCCAATGAGCTGTGATCCCGAAGTGAGACGAG 126
Oy 41 ValPheAlaAspSerIleLeuAlaAlaAlaLysAspAspTrpGluSerProProTrp 60
Db 127 GTCTTGGTGACTCCTCTTGTGTCAGACGAGGCACTGAGCTGGAGTCACTCCATAC 186
Oy 61 AsnLeuLeuTrpArgAsnAlaLeuProIleProProValLysGluProLysMetIle 80
Db 187 AACTTGCTTACAGAGATGCCCTTCCCAATTCACCTGTCAGAGCCCAAGATATCAT 246
Oy 81 ThrAsnProValThrGlyLysAspIleTrpTrpTrpGluIleGluIleLysProPheGlu 100
Db 247 ACCAACCCTGTACACCGGCAAGAGACATTTGATATGAGATGAGATCAAGCCATTTCAG 306
Oy 101 GluArgIleLysProThrLeuArgProAlaThrLeuValGlyTrpAspGlyMetSerPro 120
Db 307 CAAAGGATTTACCCACCTTGGCGCTGACCTGCTGCTGAGATGAGATGAGATGAGCT 366
Oy 121 GlyProThrPheAsnValProArgGlyThrGluThrValValArgPheIleAsnAla 140
Db 367 GGTCTTACTTTCATGTGTTCCAGAGAGAGAGACTGTAGTTCATCAACATATGCC 426

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OY 141 ThrValGluAsnSerValHisLeuHisGlySerProSerArgAlaProPheAspGlyTrp 160
 DB 427 ACCGTGAGAACTCGGTCCATCTGCAGGGCTCCCATCCGCTGCCCTTTCGATGGTGG 486
 OY 161 AlaGluAspValThrPheProGlyGlyTrpLysAspPyrTrpPheProAsnTrpGlnSer 180
 DB 487 GGTGAAGATGTAACCTTCCGCGAGTACAAAGATTACTACTTCCCACTCAATCC 546
 OY 181 AlaArgLeuLeuTrpPyrHisAspHisAlaPheMetLysThrAlaGluAsnAlaTrpPhe 200
 DB 547 GCCCGCTTCTGGTGACATGACACCGCTTTCATGAAGCTGAGAAATGCCCTACTT 606
 OY 201 GlyAlaAlaGlyAlaTrpLysLeuAsnAspGluAlaGluAspAlaLeuGlyLeuProSer 220
 DB 607 GGTGAGGCTGGCGGCTCAATTAATCAAGACGAGCGTGAAGATGCTCGCTTCTCTAG 666
 OY 221 GlyTrpGlyGluPheAspIleProLeuIleLeuThrAlaLysTrpTrpAsnAlaAspGly 240
 DB 667 GGTATGAGGAGTTCATATCCCTGATCTGACGCGCAAGTACTATTAACGCCGATGGT 726
 OY 241 ThrLeuArgSerThrGluGluGluAspGluAspLeuTrpGlyAspValIleHisLysAsn 260
 DB 727 ACCCTGCTTCCAGCCAGGAGGTGAGACACGAGCTGTGGAGATGTCAATCCATGTCAC 786
 OY 261 GlyAlaProTrpProPheLeuAsnValGlnProArgLysTrpArgPheArgPheLeuAsn 280
 DB 787 GGCAGGCCATGGGCTTCTTAAACGTCCAGCCCGCAAGTACCGTTCCGATTCCTCAAC 846
 OY 281 AlaAlaValSerArgAlaTrpLeuLeuTrpLeuValArgTrpSerProAsnValArg 300
 DB 847 GGTGCGGTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 906
 OY 301 IleProPheGluValIleLeuAspAlaGlyLeuLeuGlnAlaProValGlnTrpSer 320
 DB 907 ATTCTTCCAAAGTCAATGCTCTGATGGTGTCTCTTCCAAACCCCGTTCAGACTCT 966
 OY 321 AsnLeuTrpLeuAlaValAlaGluArgTrpGlyIleIleIleAspPheThrAsnPheAla 340
 DB 967 AACCTCTACTTGGCTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1026
 OY 341 GlyGlnThrLeuAspLeuArgAsnValAlaGluThrAsnAspValGlyAspGlu 360
 DB 1027 GGCAGACTCTGACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1086
 OY 361 TyrAlaArgThrLeuGluValMetArgPheValSerSerGlyThrValGluAsnAsn 380
 DB 1087 TACGCTGCGACTCTGAGGTGATGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1146
 OY 381 SerGlnValProSerThrLeuArgAspValProPheProHisLysGluGlyProAla 400
 DB 1147 AGCCAGGTCCTCCCTCCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1206
 OY 401 AspLysHisPheLysPheGluArgSerAsnGlyHisTrpLeuIleAsnAspValGlyPhe 420
 DB 1207 GACAGACACTTAAGTTTACGACAGCAACGACACTTACCTGATCAACATGTGGCTTT 1266
 OY 421 AlaAspValAsnGluArgValLeuAlaLysProGlnLeuGlyThrValGluValTrpGln 440
 DB 1267 GCCGATGTCAATGAGGTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1326
 OY 441 LeuGluAsnSerSerGlyLysTrpSerHisProValHisIleHisLeuValAspPheLys 460
 DB 1327 CTCGAGAACTCTCTGAGGCTGAGGACCAACCCGTCACATTCCTTGTGACTTCAAG 1386
 OY 461 IleLeuLysArgThrGlyLysArgGlyGlnValMetProTrpGlnSerAlaGlyLeuLys 480
 DB 1387 ATCCCTCAACGCAACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1446
 OY 481 AspValValTrpLeuGlyArgGlyGlyTrpLeuThrIleGluAlaHisTrpGlnProTrp 500
 DB 1447 GATGTGCTGTGTGGGAGGGGTGAGACCTGACCATGAGGCGCCACTACCAACCTG 1506
 OY 501 ThrGlyAlaTrpMetTrpHisCysHisAsnLeuIleHisGluAspAsnAspMetLeuAla 520

DB 1507 ACTGAGCTTACTATGTGGGCACTGTCAACACCTCATTCAGAGATTAACGACATGAGCT 1566
 OY 521 ValPheAsnValThrAlaMetGluGlyLysGlyTrpLeuGlnGluAspPheGluAspPro 540
 DB 1567 GTATTCACGTCAACCCCATGAGGAGAAAGGATATCTTCAGAGGACTTCGAGGACCCC 1626
 OY 541 MetAsnProLysTrpArgAlaValProTrpAsnArgAsnAspPheHisAlaArgAlaGly 560
 DB 1627 ATGAAACCCCAAGGGGCGCGCTTCTTCAACCGCAACGACTTCATGCTCGCGCTGGA 1686
 OY 561 AsnPheSerAlaGluSerIleThrAlaArgValGlnGluLeuValAlaGluGlnGluProTrp 580
 DB 1687 AACTTCTCGCGGAGTCCATCACTGCGCGAGTGCAGAGCTGGCGCAGAGAGCCGTAC 1746
 OY 581 AsnArgLeuAspGluIleLeuGluAspLeuGlyIleGluGln 594
 DB 1747 AACCGCTCGATGATCCTGAGGATCTTGGATGAGAG 1788
 RESULT 4
 AAL47584
 ID AAL47584 standard; cDNA; 1791 BP.
 XX
 AC AAL47584;
 XX
 DT 13-SEP-2002 (first entry)
 XX
 DE S chartarum phenol oxidizing enzyme cDNA.
 XX
 KW phenol oxidizing enzyme; fungus; redox reaction; detergent;
 KM paper industry; pulp industry; textile; food industry; gene; ss.
 XX
 OS Stachybotrys chartarum.
 XX
 FH Key Location/Qualifiers
 FT CDS 7..1791
 FT /*tag- a
 FT /product- "phenol oxidizing enzyme"
 XX
 PN US6399329-B1.
 XX
 PD 04-JUN-2002.
 XX
 PF 21-DEC-1999; 99US-0468578.
 XX
 PR 12-DEC-1998; 98US-0220871.
 PR 23-JUN-1999; 99US-0338723.
 XX
 PA (GENV) GENENCOR INT INC.
 XX
 PI Wang H, Bodie EA;
 XX
 DR WPI: 2002-498835/53.
 DR P-PSDB: AAO18210.
 XX
 PT New polynucleotides encoding phenol oxidizing enzymes, useful for
 PT preventing the transfer of dyes in solution from one textile to another
 PT during detergent washing -
 XX
 PS Disclosure: Fig 5; 37pp; English.
 XX
 CC The present invention provides the protein and coding sequences of phenol
 CC oxidizing enzymes from Stachybotrys chartarum, Bipolaris spiciferia and
 CC Curvularia pallescens. These enzymes are useful in the textiles, paper,
 CC pulp, detergent and food industries. In particular they are useful for
 CC preventing the transfer of dyes in solution from one textile to another
 CC during detergent washing (dye transfer inhibition). The present sequence
 CC is the S. chartarum phenol oxidizing enzyme cDNA.
 XX
 SQ Sequence 1791 BP; 380 A; 551 C; 451 G; 409 T; 0 other;
 Alignment Scores: 3.68e-303 length: 1791
 Pred. No.:

Score: 3189.00 Matches: 594
Percent Similarity: 100.00% Conservatave: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 24 Gaps: 0

US-10-080-233-2 (1-594) x AAL47584 (1-1791)

QY 1 MetLeuPheLysSerThrPglInLeuAlaAlaSerGlyLeuLeuSerGlyValIleuGly 20
DB 7 ATGGTGTTCAGATCATGCGCACTGCGACAGCCCTCGGGCTCTCTGTGGATCTCTCGGC 66
QY 21 IleProMetAspThrGlySerHisProIleGluAlaValAspProGluValIleuThrGlu 40
DB 67 ATCCGATGGACACCGGACCGACCCCATGTAGAGCTGTGTATCCGAGTGAAGACTGAG 126
QY 41 ValPheAlaAspSerIleuLeuAlaAlaIleGlyAspAspAspTrpGluSerProTrp 60
DB 127 GTCTTCGCTGACTCTCTCTCTGTCGACAGCGAGTACGACTGGAGTCACTTCATAC 186
QY 61 AsnLeuLeuTyArgAsnAlaLeuProIleProProValIysGlnProIysMetIleIle 80
DB 187 AACGTGCTTACAGGAATAGCCCTGCAATTCACCTGTCAGACAGCCCAAGATGATCAT 246
QY 81 ThrAsnProValIleThrGlyLysAspIleTrpTyrgIuIleGluIleLysProPheGln 100
DB 247 ACCAACCCCTGTACCGGACGACATTTGTACTATGATGATGATGATGATGATGATGAT 306
QY 101 GlnArgIleTyProThrLeuArgProAlaThrLeuValIleTyArgAspIleMetSerPro 120
DB 307 CAAGGATTTACCCCACTTGGCCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 366
QY 121 GlyProThrPheAsnValProArgGlyThrGluThrValValArgPheIleAsnAla 140
DB 367 GGTCTCTCTCTCATGTGTCCAGAGAACAGACTGATGATGATGATGATGATGATGATGAT 426
QY 141 ThrValGluAsnSerValHisLeuHisGlySerProSerArgAlaProPheAspGlyTrp 160
DB 427 ACCGTGAGAACTGGTGCATCTGACAGGCTCCCATCGCTGCTGCTGCTGCTGCTGCTG 486
QY 161 AlaGluAspValIleThrPheProGlyIleTyrgLysAspTyrgPheProAsnTyrgGlnSer 180
DB 487 GCTAAGATGTGACTTCCCTGCGGAGTACAAAGATTTCTACTTTCCCACTTACCAATCC 546
QY 181 AlaArgLeuLeuTrpTyrgHisAspHisAlaPheMetIleTyrgAlaGluAsnAlaTyrgPhe 200
DB 547 GCCCGCTCTGTGGTACAGTACAGCACCGCTTTCATGAAGACTGTGAGAAATGCTACTTT 606
QY 201 GlyIleAlaGlyAlaTyrgIleIleAsnAspGluAlaGluAspAlaLeuGlyLeuProSer 220
DB 607 GGTGAGGCTGGCGCTTACATTATACGACGAGGCTGAGATGCTTCTGCTGCTTCTCTAGT 666
QY 221 GlyTyrgLysGluPheAspIleProLeuIleLeuThrAlaTyrgTyrgTyrgAlaAspGly 240
DB 667 GGCATATGGCCAGTTCGATATCCCTGATCTGTAGCGGCAAGTCTATTAAGCCGAGTGT 726
QY 241 ThrLeuArgSerThrGluGlyGluAspGlnAspLeuTrpGlyAspValIleHisValAsn 260
DB 727 ACCGTGCTTGCAGCGAGGTGAGAGACAGCACTGTGGAGATGTCATCATCATCATCAT 786
QY 261 GlyIleProTrpProPheLeuAsnValGlnProArgTyrgTyrgArgPheArgPheLeuAsn 280
DB 787 GGAAGAGCCAGGCTTCTTAAAGTCCAGCCCGCAAGTACCTTTCCGATTCCTCTCAAC 846
QY 281 AlaAlaValSerArgAlaTrpLeuLeuTyrgLeuValArgThrSerSerProAsnValArg 300
DB 847 GCTCCGCTGTCTGCTGTGCT 906
QY 301 IleProPheGlnValIleAlaSerAspAlaGlyLeuLeuGlnAlaProValGlnThrSer 320
DB 907 ATTCTTTCCAAGTATGCTGCTGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 966
QY 321 AsnLeuTyrgLeuAlaValAlaGluArgTyrgIleIleIleIleAspPheThrAsnPheAla 340

DB 967 AACCTACCTTGGCTGTGGCGAGCGTTACAGATCATATTGACTTCCACCACCTTGTCT 1026
QY 341 GlyIleProLeuAspLeuArgAsnValAlaGluThrAsnAspValGlyAspGluAspGly 360
DB 1027 GGCAGACTCTTGCACCTGCGCAACGTTGTGTAGACCAAGATGTGGGAGAGAGATGAG 1086
QY 361 TyraIleArgThrLeuGluValMetArgPheValValSerSerGlyThrValIleGluAspAsn 380
DB 1087 TACGCTGCACCTTCGAGAGTATGCGCTGTCTGTCTGTCTGTCTGTCTGTCTGTCTGTCT 1146
QY 381 SerGlnValProSerThrLeuArgAspValProPheProProHisLysGlyIleProAla 400
DB 1147 AGCCAGGTCCCTCCACTCTCTGACACTTCTTCTCTCTCTCTCTCTCTCTCTCTCTCT 1206
QY 401 AspIleHisPheLysPheGluArgSerAsnGlyIleTyrgLeuIleAsnAspValGlyPhe 420
DB 1207 GACAAAGCACTTCAAGTTTGAACGACAGCAACGACACTACCTGATCAACGATGTGGCTTT 1286
QY 421 AlaAspValAsnGluArgValIleuAlaLysProGluLeuGlyThrValGluValTrpGlu 440
DB 1267 GCCATATGTCATGAGCGGTCTCTGCGCAAGCCGAGCTCGGACCGTTGAGTGTGGAG 1326
QY 441 LeuGluAsnSerSerGlyIleTrpSerHisProValHisIleHisLeuValAspPheLys 460
DB 1327 CTCGAGAACTCTCTGAGGCTGAGGACCCCTCCACATTCACCTTGTGACTTCAAG 1386
QY 461 IleLeuLysArgThrGlyIleArgGlyValGlnValMetProTyrgGluSerAlaGlyLeuLys 480
DB 1387 ATCTCAAGCCCACTGCTGGTGTGCTGCGCAAGCTCATGCTTACGATGTGCTGTGCTTAA 1446
QY 481 AspValValTrpLeuGlyArgGlyIleThrLeuThrIleGluAlaHisTyrgLleProTrp 500
DB 1447 GATGCTGCTGTGGTGGGAGGAGTACAGCCCTGACATTCAGAGCCCACTTACCAACCTGG 1506
QY 501 ThrGlyAlaTyrgMetTrpHisCysHisAsnLeuIleHisGluAspAsnAspMetAla 520
DB 1507 ACTGAGCTTACATGTGACATGTACCACTCTCATTCACGAGGATTAACGATATGAGCT 1566
QY 521 ValPheAsnValIleThrAlaMetGlyIleGlyIleTyrgLeuGlnGluAspPheGluAspPro 540
DB 1567 GTATTCAAGCTGACCCCATGAGAGAGAGAGATATCTTACGAGAGACTTGAAGACCCC 1626
QY 541 MetAsnProLysTrpArgAlaValProTyrgAsnArgAsnAspPheHisAlaArgAlaGly 560
DB 1627 ATGAACCCCAAGTGGCGGCGCTTCTTCAACCGCAACGACTTCCATGCTCGCGCTGGA 1686
QY 561 AsnPheSerAlaGluSerIleThrAlaArgValGlnGluLeuAlaGluGlnGluProTrp 580
DB 1687 AACTTCTCCCGCGAGTCCATCATGCGCGAGTGAAGAGCTGGACGACGACGACCCGTAC 1746
QY 581 AsnArgLeuAspGluIleLeuGluAspLeuGlyIleGluGln 594
DB 1747 AACCGCTCGATGATGATCTTGGAGATCTTGGAAATCCAGAGAG 1788

RESULT 5
ID ABA92911 standard; DNA; 7248 BP.
XX ABA92911:
XX 09-APR-2002 (first entry)
XX
XX Stachybotrys chartarum laccase gene.
XX DE
XX laccase; enzyme; blue copper oxidase; fungal; oxidation; reduction;
XX KW copper; metal cofactor; gene; plant; ds.
XX
XX Stachybotrys chartarum.
XX OS
XX
XX PN W0200196543-A2.
XX PD 20-DEC-2001.

XX 14-JUN-2001; 2001WO-US19174.
PF
XX

PR 15-JUN-2000; 2000US-211732P. *for loto*
XX
XX (PROD-) PRODIGENE INC.
PA (GENV) GENENCOR INC.
XX

PI Hood E, Howard JA, Bailey M, Van Gastel FJC, Ward M, Wang H;
XX Woodard S;
XX

DR WPI: 2002-090204/12.
XX

PT Improving recovery of active enzyme e.g. laccase, which requires
XX transitional metal cofactor e.g. copper for activity, from a plant, by
XX introducing plant nucleotide sequences encoding the enzyme and exposing
PT it to cofactor

Example 5; Fig 16A-E; 81pp; English.

CC The present invention describes a method for improving the recovery of
CC an active enzyme from a plant where the enzyme requires a transitional
CC metal cofactor for activity. The method comprises introducing into the
CC plant nucleotide sequences encoding the enzyme and exposing the enzyme
CC to the metal cofactor. The method is useful for improving recovery of
CC active enzyme which requires a transitional metal cofactor for activity,
CC preferably for improving recovery of active laccase which requires
CC copper for activity. The method can be used for improving recovery of
CC active organophosphate hydrolase (OPH, E.C. 3.1.8.1) which requires
CC zinc, nickel, cobalt or manganese for activity, where the method further
CC comprises adding bicarbonate ion salt. The present sequence encodes the
CC fungal *Stachybotrys chartarum* laccase enzyme. Laccases are also called
CC blue copper oxidases and use copper to accept and donate electrons in
CC the oxidation and reduction of substrates.

SQ Sequence 7248 BP; 1928 A; 1744 C; 1579 G; 1997 T; 0 other;

Alignment Scores:

Pred. No.:	2, 58e-302	Length:	7248
Score:	3189.00	Matches:	594
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	100.00%	Indels:	0
DB:	24	Gaps:	0

US-10-080-233-2 (1-594) x ABA92911 (1-7248)

1 MetLeuPheLysSerTrpGlnLeuAlaAlaAlaSerGlyLeuLeuSerGlyValLeuGly 20
5198 ATGCTGTTCAAGTCATGACGACGACGACGCTCCGGGCTCTGTCGAGTCCCTCGG 5257
21 IleProMetAspThrGlySerHisProIleGluAlaValAspProGluValIleThrGlu 40
5258 ATCCCGATGGACACGGGACCAACCCATTGAGGCTGATGCCCACTGGAAGACTGTG 5317
41 ValPheAlaAspSerLeuLeuAlaAlaIleGlyAspAspAspTrpGlnSerProProtyr 60
5318 GCTTCGCTGACTCCCTCTCTGCTGCTGACAGGCGATGACGACTGGAGTCACTTCATAC 5377
61 AsnLeuLeuTrpArgAsnAlaLeuProIleProProValIleGlnProIleMetIleIle 80
5378 AACTTGCTTTACAGAAATGCTCCATTCACACGTCACAGAGCCCAAGATGATCATT 5437
81 ThrAsnProValThrGlyLysAspIleTrpTyrTyrGluIleGluIleLysProPheGln 100
5438 ACCAAGCCCTGTACCGGACGAGACATTGTGCTATGATGATGATGATGATGATGATGAT 5497
101 GlnArgIleTrpProThrLeuArgProAlaThrLeuValGlyTyrAspGlyMetSerPro 120
5498 CAAAGATTTTACCACCTTGGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 5557
121 GlyProThrPheAsnValProArgGlyThrGluThrValValArgPheIleAsnAla 140

5558 GGTCTACTTTCAATGATTCCTCCAGAGACAGACATGTAGTTAGTTATCAACAAATGCC 5617
141 ThrValGluAsnSerValHisLeuHisGlySerProSerArgAlaProPheAspGlyTrp 160
5618 ACCGTGAGAAACGGGTCCATTCGACGGGTCCCACTGGCTGCCCTTCGATGGTTGG 5677
161 AlaGluAspValThrPheProGlyGlyTyrLysAspTyrThrPheProAsnTyrGlnSer 180
5678 GCTGAAGATGTGACTTCCCTGCGAGTACAGAGATTTACTACTTCCCAATCTCAATCC 5737
181 AlaArgLeuLeuTrpTyrHisAspHisAlaPheMetLysThrAlaGluAsnAlaTyrPhe 200
5738 GCCGCTCTCTGTGATACCATGACACCGCTTTCATGAGCTGCTGAGATGGCTACTTT 5797
201 GlyGlnAlaGlyAlaTyrIleIleAsnAspGluAlaGluAspAlaLeuGlyLeuProSer 220
5798 GGTACGGCTGGCCCTTCAATATCAACAGACGAGGCTGAGAGTCTCGGCTCTCTAGT 5857
221 GlyTyrGlyGluPheAspIleProLeuIleLeuThrAlaLysTyrTyrAsnAlaAspGly 240
5858 GGCTATGGGAGTTCATATCTCTGATCTTACGCGCCAAAGTACTATTAACGCGATGGT 5917
241 ThrLeuArgSerThrGluGlyLysAspGlnAspLeuTrpGlyAspValIleHisValAsn 260
5918 ACCCTCGTTCGACGAGGAGTGAGACAGGACCTGTGGGAGATGTCATCTGTCACAC 5977
261 GlyGlnProTrpProPheLeuAsnValGlnProAlaTyrTyrArgPheArgPheLeuAsn 280
5978 GGACACCACTGGCTTCTTAACTGACGAGCCCGCAAGACGTTCCGATCTCCATCAC 6037
281 AlaAlaValSerArgAlaThrLeuLeuTyrLeuValArgThrSerSerProAsnValArg 300
6038 GCTGCGGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 6097
301 IleProPheGlnValIleAlaSerAspAlaGlyLeuLeuGlnAlaProValGlnThrSer 320
6098 ATTCCTTTCOAAGTCATGCTGCTGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 6157
321 AsnLeuTyrLeuAlaAlaAlaGluArgTyrGluIleIleIleAspPheThrAsnPheAla 340
6158 AACCTTACCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 6217
341 GlyGlnThrLeuAspLeuArgAsnValAlaGluThrAsnAspValGlyAspGluAspGlu 360
6218 GCGCAGACTTTCACCTGCGCAACGTTGCTGAGACCAAGATTCGCGCAGCAGATGAG 6277
361 TyrAlaArgThrLeuGluValMetArgPheValIleSerSerGlyThrValGluAspAsn 380
6278 TAGCTCGACACTCTCGAGGATGCGCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 6337
381 SerGlnValProSerThrLeuArgAspValProPheProProHisLysGluGlyProAla 400
6338 AGCAGAGTCCCTCCCACTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 6397
401 AspLysHisPheLysPheGluArgSerAsnGlyHisTyrLeuIleAsnAspValGlyPhe 420
6398 GACAGACATTCAGATTGTAACGACCAACGACACTACTGATCAACATGTGGCTTT 6457
421 AlaAspValAsnGluArgValLeuAlaLysProGluLeuGlyThrValGluValTrpGlu 440
6458 GCCGATGTCATGAGGCTGCTGCGCAAGCCGAGCTGCGGACCTTGAGGTCTGGAG 6517
441 LeuGluAsnSerSerGlyGlyTyrPheSerHisProValHisIleHisLeuValAspPheLys 460
6518 CTCGAGAACTCTCTGAGAGCTGAGACCAACCCGCTCAATTCACCTTGTGCTTCAAG 6577
461 IleLeuLysArgThrGlyGlyArgGlyGlnValMetProTyrGluSerAlaGlyLeuLys 480
6578 ATCTCTACAGCAACTGT 6637
481 AspValValTrpLeuGlyArgGlyGlyGluThrLeuThrIleGluAlaHisTyrGlnProTrp 500
6638 GATGTCTGT 6697

QY 129 YTHGGLUTHRVALVALARGPHEILEASNALATHRVALGLUASNSERVALHISLEUHI 149
 DB 550 AACAGAGACTGATAGTAGTTCATCAACAAATGCCACCGTGAGAACTGGTCCATCTGCA 609
 QY 149 SGYLSERPROSERATGALAPROPHENASPGLYTPRALAGLUASPVALLHRRPHEGGLYGL 169
 DB 610 CGGCTCCCATCGGCTGGCCCTTTCGATGGTGGCTTCAAGATGGACCTTCCCGGGGA 669
 QY 169 UTLYLASPTLYTYRPHENPROASNLYGINSERIALARGLEULEUTPRYTHIASPHI 189
 DB 670 GTACAGGATTAACACTTCCCACTACCAATCCGCCCTTCTGTGTACATGACCA 729
 QY 189 SALAPHENELYS 193
 DB 730 CGCTTTCATGAA-GGATGCTACGAGCCTTATCTTCTGGCTACCTTTGGCTAACCA 788
 QY 194 -----THRALAGLUASNALATYRPHEGLYLINALAGLYALTYRLEILEAS 209
 DB 789 CTTCCTTTGAGACTGCTGAGAAATGCTACTTGGTCAGGCTGGCCCTCATATTCAA 848
 QY 209 NASPGLUAGLUASPALALAGLYLEUPROSERGLTYRGLYGLUPHENASPILEPROLE 229
 DB 849 CGAGAGGCTGAGATGCTCTCGCTTCTCTAGTGGCTATGGCGAGTTCGATATCTCT 908
 QY 229 UILELEUTHRALALASTYTYRASNALAASPGLYTHRLEUARGSERTHRGLUGLYLUAS 249
 DB 909 GATCCTGAGCGCCAAGTACTATAACGCCGATGGTACCTGCGGTGACCGAGGGTGAGGA 968
 QY 249 PGLIASPLEUTRPGLYASPVALLIETHIASNLGLYINPROTRPPROPHLEUASVVA 269
 DB 969 CCAGAGACTGTGGGAGATGTCATTCATGCAACGAGCAGATGGCCCTTTCCTTAACGT 1028
 QY 269 IGLINPROARGLYSTRARGPHEARGPHELEUASNALALVALSERATGALATRPLEULE 289
 DB 1029 CCAGCCCCGAGAACTGTTCCGATTCCTCAACGCTCCGCTGTCTGCTTGGCTCT 1088
 QY 289 UTYRLEUVALARGTHRSESRPROASNVALARGILEPROPHGLVALILEALASERAS 309
 DB 1089 CTACCTGCTGAGACACACTCTCCCAACGTAGAAATTCCTTCCAAAGTCATTTGCTCGA 1148
 QY 309 PALAGLYLEULEUGLINALPROVALGLNTHRSERASLEUTRYLEUALVALALAGLUAR 329
 DB 1149 TGTGGTCTCTTCAAGCCCGCTTCAGACCTTAACCTTGTGTGGCGGACCG 1208
 QY 329 GTYRGLULEILEILE----- 334
 DB 1209 TTAGAGATCATTTTGTGTATGCCCTCCCTCTCAGCAATGAGTCAGAACTCTAAGACT 1268
 QY 335 -----ASPHERTHRASNPHENALAGLYGLNTHRLEUASPLEUARASVALALAGL 351
 DB 1269 AACACTTGTAGACTTCAACCACTTGTGGCCAGACCTTGTACCTGCGCAACGTGTGTA 1328
 QY 351 UTHRASNAPVALAGLYASPGLUASPGLUUTYRALARGTHRLEUGLVALMETATRPHVA 371
 DB 1329 GACCAAGAGATGTCGGCGAGAGATGATACGCTGCGACTTCCAGGAGGATGCGCTTCT 1388
 QY 371 IVALSERSEGLYTHRVALGLUASPASNSERGLNVALPROSETRHLEUARGASPVALLPR 391
 DB 1389 CGTCAAGCTCTGCACTGTGGAGAACACAGCCAGTCCCTCCCACTCTCCCTGACGTTCC 1448
 QY 391 OPHERPROHISLYSGLYGLYPTROALASRPLYSHPHELYSPEGUARGSERASNL 411
 DB 1449 TTTCCCTCTCACAAGGAGAGCCCGCCGACAAACACTTCAAGTTTGAACACAGCAACGG 1508
 QY 411 YHISTYRLEULEASNPVALAGLYPHEALASPVALLASNLARGVALLEUALALYSPT 431
 DB 1509 ACACCTACCTGATCAACAGATGTTGGCTTGGCATATAGGCTGCTCGGCCAACGCC 1568
 QY 431 OGILEUGLYTHRVALGLUVALTRPGLULEUGLUASNSERSEGLYGLYTPRSEHISPR 451
 DB 1569 CGAGCTGGGACCGTTGAGTCTGGGAGCTGAGAACTCTCTGAGGCTGGACCAACCC 1628

QY 451 OVALHISILIEHISLEUVALASPPHELYSILEULEYSAARGTHRGLYARGGLYGLNVA 471
 DB 1629 CGTCCACATTCACCTGTTGACTTCAAGATCTCAAGCGAAGCTGGTGGTGGCAGAGT 1688
 QY 471 IMETPROTYRGLINUSERIALAGLYLEULYASPVALLTRPLEUGLYATGGLYGLUTHLE 491
 DB 1689 CATGCCCTACAGACTGCTGTGCTTAAAGATGTGCTGGTGGGACAGGGGTGAGACCT 1748
 QY 491 UTHRLEGLUALHISTYRGLINPROTRPTTHRGLYALATYRMETRPHISCSHISASNLE 511
 DB 1749 GACCATGAGGCCCACTACCAACCTGGACTGGAGACTTACATGTGGCACTTCAACACT 1808
 QY 511 UILEHISGLUASPASNPASPMETLALVALPHEASNVALTHRALMETGLUGLYSGI 531
 DB 1809 CATTCACAGAGATAACGACATGATGGCTGATATCAAGCTACCGCCATGAGAGAGAGG 1868
 QY 531 YTYRLEUGLNUASPPHEGLUASAPPROMETASNPOLYSTTRPRALVALPROTYRAS 551
 DB 1869 ATATCTTCAAGAGAGCTTCGAGAACCCCATGAACCCCAAGTGGCGCCGCTTACAA 1928
 QY 551 NARGASNAPPHENISALARGALAGLYASNPHESERIALAGLUSERILERTHRLAARGVA 571
 DB 1929 CCGCAGACACTTCCATGCTGCGCTGGAAACTTCCCGCGAGTCCATCACTGCCAGCT 1988
 QY 571 IGLINLEUVALAGLUGLNUPTROTYRASNARGLEUASPGLUILEUGLUASPLEUGI 591
 DB 1989 GCAGAGGCTGGCCGAGCAGAGCGGTACAAACCGCTCGATGAGATCTCGAGATCTTGG 2048
 QY 591 YILEGLUGLU 594
 DB 2049 AATCGAGGAG 2058

RESULT 8

AA227609
 ID AA227609 standard; DNA; 2067 BP.
 AC AA227609;
 XX 16-DEC-1999 (first entry)
 DE Stachybotrys phenol oxidase coding sequence.
 XX Stachybotrys phenol oxidase compound; dye transfer prevention;
 XX phenol oxidase; enzyme; coloured compound; dye transfer prevention;
 KW fabric washing; stain bleaching; anti-dye transfer; detergent; ss.
 XX Stachybotrys chartarum.
 OS W09949020-A2.
 PN 30-SEP-1999.
 XX 23-MAR-1999; 99WO-US06327.
 PF 24-MAR-1998; 98US-0046969.
 PR 22-DEC-1998; 98US-0218702.
 PR 22-MAR-1999; 99US-0273957.
 PA (GENV) GENENKOR INT INC.
 PI Amory A, Wang H, Dhase P, Lambrechts-Rongvaux A, Wang C;
 DR WPI; 1999-591088/50.
 PT Novel enzyme for modifying coloured compounds used to prevent
 PT dye-transfer -
 XX Example 17; Fig 9; 64pp; English.
 PS This sequence encodes the Stachybotrys chartarum phenol oxidase enzyme
 CC of the invention. The invention is used to modify a coloured compound and
 CC prevent dye transfer during fabric washing, or for stain bleaching or
 CC anti-dye transfer. It is useful in the detergent, paper and pulp, textile
 CC and food industries.

XX Sequence 2067 BP; 445 A; 621 C; 500 G; 501 T; 0 other;
SQ Alignment Scores:
Pred. No.: 5,17e-290 Length: 2067
Score: 3056.00 Matches: 593
Percent Similarity: 86.70% Conservative: 0
Best Local Similarity: 86.70% Mismatches: 1
Query Match: 95.83% Indels: 91
DB: 20 Gaps: 3
US-10-080-233-2 (1-594) x AA227609 (1-2067)
QY 1 MetLeuPheLysSerTrpGlnLeuAlaAlaSerGlyLeuLeuSerGlyValLeuGly 20
DB 10 ATGCTTTAGTCAATGCAAGCACTGGCAGACGCTCCGGCTCTGTGTGAGTCTCGGC 69
QY 21 IleProMetAspThrGlySerHisProIleGluAlaValAspProGluValLysThrGlu 40
DB 70 ATCCGATGGACACCGCAGCCACCATTGAGGTGTGTGATCCGAAAGTGAAGACTGAG 129
QY 41 ValPheAlaAspSerLeuLeuAlaAlaGlyAspAspAspTrpGlnSerProProTyr 60
DB 130 GCTTCGTGACTCCCTCTCTGCTGAGAGGCGATGAGACAGTCCGATCCATAC 189
QY 61 AsnLeuLeu-----Tyr 64
DB 190 AACTTCCTTTACAGTGAGACACACCTGCCACTGTTTCCCGATACCTAACTCTTAT 249
QY 65 ArgAsnAlaLeuProIleProValLysGlnProLysMet----- 78
DB 250 AGGAATGCCCCGCAATTCACCTGTCAGACAGCCCAAGATGTATGATTTGATTTCTA 309
QY 79 -----IleIleThrAspProValThrGly 87
DB 310 CGAAGCACTCGGCCCGCACTAATGTATTCTAGACATTAACACCTGTCACGCGCAA 369
QY 87 sAspIleTrpTyrTyrGluIleGluIleLysProPheGlnGlnArg----- 102
DB 370 GGCACATTGGTACTATGAGATGAGATCAAGCATTTTCAGCAAAAGGTGAGTTGGCTAG 429
QY 103 -----IleTyrProThrLeuArgP 109
DB 430 AAACCTTGTGTAATTAATCATGTGTACTGACCCCTTTCAGATTTCACCCACTTGGCGCC 489
QY 109 oAlaThrLeuValGlyTyrAspGlyMetSerProGlyProThrPheAsnValProArg 129
DB 490 TGCACACTCTGTCGGCTAGAGTGGCAYGAGCCCTGGTCTACTTCAATGTTCCAGAGG 549
QY 129 yThrGluThrValValArgPheIleAsnAsnAlaThrValGluAsnSerValHisLeu 149
DB 550 AACAGAGACTGATAGTTAGTTCAATCAACATGCGACCGTGAGAACTCGGTCCATTCGA 609
QY 149 sGlySerProSerArgAlaProPheAspGlyTyrPalGluAspValThrPheProGly 169
DB 610 CCGCTCCCATGCGCGGCCCTTTCATGTTGGGCTGAAGATGATCACTTCCCTGGCGCA 669
QY 169 uTyrLysAspTyrTyrPheProAsnTyrGlnSerAlaArgLeuLeuTrpTyrHisAsp 189
DB 670 GTACAGAGATTAATACTTCCCACTACCAATCCGCCCGCTTGTGTGACCATGACCA 729
QY 189 sAlaPheMetLys----- 193
DB 730 CCCTTTCATGAA-GGATGCTAGAGCCCTTATCTTCTGGTACCTTGGTAAACAA 788
QY 194 -----ThrAlaGluAsnAlaTyrPheGlyGlnAlaGlyAlaTyrIleLeu 209
DB 789 CTTCCTTTCGTAGACTGCTGAGAAATCCCTACTTGGTTCAGGCTGCGCTACATTAACA 848
QY 209 nAspGluAlaGluAspAlaLeuGlyLeuProSerGlyTyrGlyGlnPheAspIlePro 229
DB 849 CCAAGGCTGAGAGATGCTCTGCTGCTCTTCTAGTGGCTATGGGAGATTGCAATATCCCTCT 908

QY 229 uIleLeuThrAlaLysTyrTyrAsnAlaAspGlyThrLeuArgSerThrGluGluAs 249
DB 909 GATCTGACGCGCCAACTACTATTAACGCCGATGGTACCTCTGTTCCAGCCAGGGGTGAGA 968
QY 249 pGlnAspLeuTrpGlyAspValIleHisValAsnGlyGlnProTyrProPheLeuAsn 269
DB 969 CCAGAGACTGTGGGAGATGTCAATGCAATGCAAGGAGACCAATGGCTTCTCTTAACG 1028
QY 269 LglnProAlaGlyLysTyrArgPheArgPheLeuAsnAlaAlaValSerArgAlaTrpLeu 289
DB 1029 CCAGCCCCGCAATACCGTTCCGATTCCTCAACGCGTCCGTCTGCTGCTGCTCTCT 1088
QY 289 uTyrLeuValArgThrSerSerProAsnValArgIleProPheGlnValIleAlaSer 309
DB 1089 CTACCTCTGAGGACCAAGCTCTTCCAAAGTCACAAATTCCTTTCAAAGTCACTTCCCTG 1148
QY 309 pAlaGlyLeuLeuGlnAlaProValGlnThrSerAsnLeuTyrLeuAlaValAlaGlu 329
DB 1149 TGCTGGTCTCTCAAGCCCCGCTCAGACTCTTAACCTCTACCTTGTGTCGAGCG 1208
QY 329 gTyrGluIleIleIle----- 334
DB 1209 TTACGAGATCATTAATGTATGCTATGCCCTCCCTCAGCAATGACTCAAGAACTGAAG 1268
QY 335 -----AspPheThrAspPheAlaGlyGlnThrLeuAspLeuArgAsnValAla 351
DB 1269 AACACTGTGAGACTTACCACTCTTGTGGCCAGACTCTTGACCTGCGCACTGTGCTGA 1328
QY 351 uThrAsnAspValGlyAspGluAspGluTyrAlaArgThrLeuGluValMetArgPhe 371
DB 1329 GACCAAGATGTGGGAGAGAGATGATGAGCTCCAGCTCGAGAGTGTATGGCTTCGT 1388
QY 371 lValSerSerGlyThrValGluAspAsnSerGlnValProSerThrLeuArgAspVal 391
DB 1389 CGTCACCTCTGGAGCTGTGAGAACCAACACCGTCCCTCCACTCTCTCGTACCTTC 1448
QY 391 oPheProProHisLysGluGlyProAlaAspLysHisPheLysPheGluArgSerAsn 411
DB 1449 TTTCCTCTCTCAAGAGAGGCCCGCCGCAAGCACTTCAATTTGAACGCAAGCAAG 1508
QY 411 yHisTyrLeuIleAsnAspValGlyPheAlaAspValAsnGluArgValLeuAlaLys 431
DB 1509 ACACCTACCTGATCAAGCATTTGCTTGGCGATGCAATGAGACGTCCTGCGCAAGCC 1568
QY 431 oGluLeuGlyThrValGluValTrpGluLeuGluAsnSerSerGlyTyrPheHisP 451
DB 1569 CGAGCTCGGACCGTTGAGGCTGAGAGCTCGAAGCTCTCTGAGGCTGGAGCCACC 1628
QY 451 oValHisIleHisLeuValAspPheLysIleLeuLysArgThrGlyYArgGlyGln 471
DB 1629 CGTCCACATTCACCTTGTACCTTCAAGATCCTCAAGCAAGCTGGTGTGCGCAGGT 1688
QY 471 lMetProTyrGluSerAlaGlyLeuLysAspValValTrpLeuGlyArgGlyLysThr 491
DB 1689 CATGCCCTACGATCTGCTGTCTTAAGATGTCGTGTGGTGGAGGGGTGAGACCT 1748
QY 491 uThrIleGluAlaHisTyrGlnProThrPheGlyAlaTyrMetTrpHisGlyHis 511
DB 1749 GACCATGAGGGCCCACTACCAACCTGAGCTGATCATGTGGAGCTGATGACCTGACAA 1808
QY 511 uIleHisGluAspAsnAspMetMetAlaValPheAsnValThrAlaMetGluGlu 531
DB 1809 CATTCAGAGGATTAAGACATGATGGCTGATTAACAGTCAAGCCATGGAGAGAGAGG 1868
QY 531 yTyrLeuGlnGluAspPheGluAspProMetAsnProLysTrpArgAlaValProTyr 551
DB 1869 ATATCTTCAGAGAGACTTGGAGAGCCCAAGAACCCCAAGTGGCGGCGCTTCTTAACA 1928
QY 551 nArgAsnAspPheHisAlaArgAlaGlyAsnPheSerAlaGluSerIleThrAlaArg 571
DB 1929 CCGCAAGCACTTCCATGCTGCGCTGGAACCTTCTCGCGGATCCATCACTGCGCGAG 1988
QY 571 lGlnGluLeuAlaGluGlnGluProTyrAsnArgLeuAspGluIleLeuGluAspLeu 591

Db	1989	GCAGAGCTGGCCGAGCAGCGCTACACCGCTCGATGAGATCCTGGAGATCTTGG	2048
Qy	591	YIIeGlUGlU 594	
Db	2049	AATCGAGGAG 2058	
RESULT 9			
AA25728			
ID	AA25728	standard; DNA; 3676 BP.	
XX			
AC	AA25728;		
XX			
DT	05-JAN-2000	(first entry)	
DE	Stachybotrys chartarum	phenol oxidising enzyme genomic DNA.	
XX	Stachybotrys chartarum:	phenol oxidising enzyme; colour; dye;	
XX	detergent; anti-dye transfer;	stain removal; bleaching; ds.	
KW			


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DB 2243 TTACGAGATCATATGATGATGCCCTCCCTCTCAGCATGAGTCAAGAACTAGACT 2302
QY 335 -----AspPheThrAsnPheAlaGlyGlnThrLeuAspLeuArgAsnValAlaGly 351
DB 2303 AACACTTGTAGATCTCACCACACTTGTGCGCAGACTCTTGACCTCGCAACGTTGCTGA 2362
QY 351 uThrAsnAspValGlyAspGluAspGluThrAlaArgThrLeuGlnValMetArgPhe 371
DB 2363 GACCAACGATGTCGGCGAGAGAGATGATGATGCTCCACTCTCGAGAGTATGCGCTGCT 2422
QY 371 lValSerSerGlyThrValGluAspAsnSerGlnValProSerThrLeuArgAspValPr 391
DB 2423 CGTCAGCTCTGGCAGCTGTGAGAGACAGCAGCTCCCTCCACTCTCGTACCTTCC 2482
QY 391 oPheProProHisGlyGlyProAlaAspLysHisPheLysPheGluArgSerAsnGly 411
DB 2483 TTTCCCTCCACAAAGGAGGCCCGCCGACAAAGCACTTCAAGTTTGAACGCGCAACGG 2542
QY 411 lHisThrLeuLeuAsnAspValGlyPheAlaAspValAsnGluArgValLeuAlaLysPr 431
DB 2543 AACACTGCTGATCAACGATGTGGCTTGCAGATGTCATGAGCGTGTCTGCGCAAGCC 2602
QY 431 oGluLeuGlyThrValGluValThrPgluLeuGluAsnSerSerGlyGlyTrpSerHisPr 451
DB 2603 CGAGCTCGGCGACGTTGAGAGTCTGGAGCTCGAGAACTCTCTGGAGGCTGGAGCCACC 2662
QY 451 oValHisThrLeuValAspPheLysLysLeuLysArgThrGlyValArgGlyGlnVal 471
DB 2663 CCTTCACATTCACCTGTGTGACTTCAAGATCCTCAAGCAAGCTGGTGGTGGCCAGGT 2722
QY 471 lMetProTrpGluSerAlaGlyLeuLysAspValValTrpLeuGlyArgGlyGlnThrLe 491
DB 2723 CATGCCCTTACGATGCTGCTGCTTAAAGATGCTGCTGTGGAGGAGGAGACCTT 2782
QY 491 uThrThrLeuAlaHisThrGlnProThrPheGlyAlaThrMetTrpHisCysHisAsnLe 511
DB 2783 GACCATCGAGGCCCACTACCAACCTCGAGCTGAGCTTCAAGTGGCACTGTCCACAACT 2842
QY 511 uLeuHisGluAspAsnAspMetMetAlaValPheAsnValThrAlaMetGluGlnLysGly 531
DB 2843 CATTCACGAGGATACGACATGATGCTGTATTCACGCTACCGCATGGAGAGAGAGG 2902
QY 531 YThrLeuGlnGluAspPheGluAspPheMetAsnProLysTrpArgAlaValProTrpAs 551
DB 2903 AATATCTTCAGAGGACTTCGAGGACCCCATGAACCCCAAGTGGCGGCGCTTCTTACA 2962
QY 551 nArgAsnAspPheHisAlaArgAlaGlyAsnPheSerAlaGluSerThrAlaLysArg 571
DB 2963 CCGCAACGACTTCATGCTCGCGCGGAAACTTCTCCGCGAGTCCATCAGTCCGAGCT 3022
QY 571 lGlnGluLeuAlaGluGlnGluProTrpAsnArgLeuAspGluThrLeuGluAspLeuGly 591
DB 3023 GGAGAGGCTGGCGGAGAGAGAGCCGTACAAACGCGCTGATGATCTCGAGAGATCTTGG 3082
QY 591 YlleGluGlu 594
DB 3083 AATCGAGAG 3092

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RESULT 10
AA227602
ID AA227602 standard; DNA; 3677 BP.
XX
AC AA227602;
XX
DT 16-DEC-1999 (first entry)
XX
DE Stachybotrys phenol oxidase genomic sequence.
XX
KW phenol oxidase; enzyme; coloured compound; dye transfer prevention;
XX fabric washing; stain bleaching; anti-dye transfer; detergent; ss.
OS Stachybotrys chartarum.

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XX
PN W09949020-A2.
XX
PD 30-SEP-1999.
XX
PF 23-MAR-1999; 99WO-US06327.
XX
PR 24-MAR-1998; 98US-0046969.
PR 22-DEC-1998; 98US-0218702.
PR 22-MAR-1999; 99US-0273957.
XX
PA (GENEV ) GENENCOR INT INC.
XX
PI Amory A, Wang H, Dphase P, Lambrechts-Rongvaux A, Wang C;
PI WPI; 1999-591088/50.
DR P-PSDB; AAY3992.
DR
PT Novel enzyme for modifying coloured compounds used to prevent
PT dye-transfer.
XX
PS Claim 21: Fig 6; 64pp; English.
XX
CC This sequence encodes the Stachybotrys chartarum phenol oxidase enzyme
CC of the invention. The invention is used to modify a coloured compound and
CC prevent dye transfer during fabric washing, or for stain bleaching or
CC anti-dye transfer. It is useful in the detergent, paper and pulp, textile
CC and food industries.
XX
SQ Sequence 3677 BP; 822 A; 1056 C; 849 G; 947 T; 3 other;

Alignment Scores:
Pred. No.: 1.15e-289 Length: 3677
Score: 3056.00 Matches: 593
Percent Similarity: 86.70% Conservative: 0
Best Local Similarity: 86.70% Mismatches: 1
Query Match: 95.83% Indels: 91
DB: 20 Gaps: 5

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QY 1 MetLeuPheLysSerTrpGlnLeuAlaAlaLysGlyLeuLeuSerGlyValLeuGly 20
DB 1044 ATTCCTTTCAAGCATGAGGACGACGACGCTCCGGGCTCTGTGAGTCTCGGC 1103
QY 21 lLeuProMetAspThrGlySerHisProThrLeuAlaValAspProGluValLysThrGln 40
DB 1104 ATCCCGATGAGACCGCGAGCCACCCCATGAGGCTGTGATCCGAAAGTGAAGACTGAG 1163
QY 41 ValPheAlaAspSerLeuLeuAlaAlaGlyAspAspAspTrpLysProProTrp 60
DB 1164 GTCTTGGCTGACTCCTCTCTGCGAGAGGAGGAGAGACGACGACCTCCATTC 1223
QY 61 AsnLeuLeu-----Tyr 64
DB 1224 AACTTGCTTACAGTGAAGAGACACCTGCCACTGTTCCTCCGATTAATCTGTTAT 1283
QY 65 ArgAsnAlaLeuProThrProProValLysGlnProLysMet-----Tyr 78
DB 1284 AGGAATGCCCTGCCAATTCACCTGCAAGACCCCAAGATGATGTCTTGAATTTCTA 1343
QY 79 -----lleThrAsnProValThrGly 87
DB 1344 CGAAGCACTCGGCCCGCAATGATTTCTAGATCATTCACCGCTGTCACCGGCA 1403
QY 87 sAspThrProTrpGluThrGluThrLysProPheGlnArg-----Tyr 102
DB 1404 GGACATTTGTACTATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1463
QY 103 -----lleTrpProThrLeuArgPr 109
DB 1464 AACCTTGTGTAATTAATTAATGATGATGATGATGATGATGATGATGATGATGATGAT 1523

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109 oAlaThrLeuValGlyTyrAspGlyMetSerProGlyProThrPheAsnValProArg1 129
1524 TGCCCTCTCGTGGCTACGATGGCATGGCCCTGGCTACTTCAATGTTCCAGAGG 1583
129 yThrGluThrValValArgPheIleAsnAsnAlaThrValGluAsnSerValHisLeuH1 149
1584 AACAGAGCTAGTAGTTCATCAACAATGCCCGTGAGAACTGGTCCACTCCCA 1643
149 sGlySerProSerArgAlaProPheAspGlyTyrPheGluAspValThrPheProGly1 169
1644 CGGCTCCCATCGGCTGGCCCTTGGATGGTGGCTCAAGATGGACCTTCCCGGGA 1703
169 uTyrLysAspTyrTyrPheProAsnTyrGlnSerAlaArgLeuLeuTyrTyrHisAspH1 189
1704 GTACAGAGATTACTCTTCCCACTACCAATCCCGCCCTTGTGTGATCAGTACCA 1763
189 sAlaPheMetLys----- 193
1764 CGCTTTCATGAA-GGTATGCTACGAGCCTTATCTTGTGGCTACCTTGGCTAACCA 1822
194 -----ThrAlaGluAsnAlaTyrPheGlyGlnAlaGlyAlaTyrIleLeas 209
1823 CTTCCTTCTGTAGACTGTGAGAAATGCTACTTGTGTGAGCTGGCCGCTACATTATCA 1882
209 nAspGluAlaGluAspAlaLeuGlyLeuProSerGlyTyrGlyGluPheAspIleProLe 229
1883 CGAGAGGCTAGGATGCTCTCGGCTCTCTAGTGGCTATGGCGAGTTCGATATCCCTCT 1942
229 uIleLeuThrAlaLysTyrTyrAsnAlaAspGlyThrLeuArgSerThrGluGlyAs 249
1943 GATCTGACGGCCCAAGTACTATACGGCGATGATACCTGGCTGACCGAGGAGGA 2002
249 pGluAspLeuTyrPheGlyAspValIleHisValAsnGlyGlnProTyrProPheLeuAsnVa 269
2003 CCAGGACCTGTGGGAGATGATCATCATGTCACGAGCAGCATGGCTTTCCTTAAGT 2062
269 IGlNProArgLysTyrArgPheArgPheLeuAsnAlaAlaValSerAlaGlaTyrPheLeu 289
2063 CCAGCCCGCAAGTACCTTTCGATTCCTCAACGCTCCGCTGCTCTGCTGCTCT 2122
289 uTyrLeuValArgThrSerSerProAsnValArgIleProPheGlnValIleAlaSerAs 309
2123 CTACCTGCTAGGACACACTCTCCCAAGTCAAGATTCCTTCCAGTCAATGGCTCTGA 2182
309 pAlaGlyLeuLeuGlnAlaProValGlnThrSerAsnLeuTyrLeuAlaValAlaGluAr 329
2183 TGTGTGTCTCTCAAGCCCGGTCAAGACTCTTAACCTTAACCTTGTGTGCGAGCG 2242
329 gTyrGluIleIleIle----- 334
2243 TTACGAGATCATTTATGTATGCCCTCCCTCTCAGAAATGATCAAGAACTTAAGACT 2302
335 -----AspPheThrAsnPheAlaGlyGlnThrLeuAspLeuArgAsnValAlaG1 351
2303 AACACTTGTACACTTCAACCACTTGTGGCCAGACTCTTGAACCTGGCCAAAGTTGCTGA 2362
351 uThrAsnAspValGlyAspGluAspGluTyrAlaArgThrLeuGluValMetArgPheVa 371
2363 GACCAACGATGTGGCGACGAGATGATGATGATGATGATGATGATGATGATGATGAT 2422
371 lValSerSerGlyThrValGluAspAsnSerGlnValProSerThrLeuArgAspValPr 391
2423 CGTACGCTGTGGCACTGTGGAGCAACAGCCAGGTCCCTCCACTCCCTGAGAGTTCC 2482
391 oPheProHisLysGlyGluProAlaAspLysHisPheLysPheGluArgSerAsnG1 411
2483 TTTCCTCTCTACAAAGAGGCGCCGCGACAGCACTTCAAGTTTGAACGACAGCAACGG 2542
411 yHisTyrLeuIleAsnAspValGlyPheAlaAspValAsnGluArgValIleuAlaLysPr 431
2543 ACACTACCTGATCAACGATGTGGCTTGGCGATGTCAATGAGCGTGTCTGGCCAAAGCC 2602
431 oGluLeuGlyThrValGluValTyrGluLeuGluAsnSerSerGlyTyrSerHisPr 451

2603 CGAGCTCGCACACCGTTGAGTCTGGAGACTCGAGAACTCTGTGAGAGCTGAGACACCC 2662
451 oValHisIleHisLeuValAspPheLysIleLeuLysArgThrGlyArgGlyGlnVa 471
2663 GGTCCACATTCACCTTGTGACTTCAAATCTTCAAGGAACTGGTGGTGGTGGTGGTGGT 2722
471 lMetProTyrGluSerAlaGlyLeuLysAspValValThrPheGluArgGlyGluThrLe 491
2723 CATGCCCTACAGAGTGTGTGTCTTAAGATGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 2782
491 uThrIleGluAlaHisTyrGlnProTyrThrGlyAlaTyrMetThrPheLysHisAsnLe 511
2783 GACCATTCAGAGCCCACTACCAACCTGGAGTGGAGCTTACATGTGGCACTGTCAACCT 2842
511 uIleHisGluAspAsnMetMetAlaValPheAsnValThrIleMetGluGlyGlu 531
2843 CATTCACGAGATTAACGATGATGCTGTATTCACCTCACCGCATGGAGAGAGAGG 2902
531 yTyrLeuGlnGluAspPheGluAspProMetAsnProLysTyrPheAlaValProTyrAs 551
2903 ATATCTTACGAGAGACTTCGAGAACCCCATGATACCCCAAGTGGCGCGCTTCCCTTACA 2962
551 nArgAsnAspPheHisAlaArgAlaGlyAsnPheSerAlaGluSerIleThrAlaArgVa 571
2963 CCGCAACGACTTCCATGCTCGCGCTGGAATCTCTCCCGAGTCCATCACTGCGCCGAGT 3022
571 lGlnGluLeuAlaGluGlnGluProTyrAsnArgLeuAspGluIleLeuGluAspLeuG1 591
3023 GCAGAGCTGGCCGAGCAGAGCCGTACACCGCTCATAGATCTCTGGAGATCTTGG 3082
591 yIleGluGlu 594
3083 AATCAGAGAG 3092

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Job time : 451 secs

GenCore version 5.1.6
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Run on: July 3, 2003, 22:57:32 ; Search time 80 Seconds
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Perfect score: 3189
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Ygapop 10.0, Ygapext 0.5
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Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length DB	ID	Description
1	3189	100.0	1791	4	US-09-468-578-5
2	3189	100.0	1791	4	US-09-218-702-1
3	3056	95.8	2067	4	US-09-218-702-5
4	3056	95.8	3677	4	US-09-468-578-1
5	3056	95.8	3677	4	US-09-218-702-3
6	1870	58.6	2063	4	US-09-468-578-6
7	1868	58.6	2905	4	US-09-468-578-3
8	1620.5	50.8	1958	4	US-09-401-476-1
9	1620.5	50.8	2095	4	US-09-401-476-3
10	666.5	20.9	858	4	US-09-468-578-8
11	409.5	12.8	969	4	US-09-134-001C-109
12	200.5	6.3	2249	3	US-08-814-052-19

13	200.5	6.3	2300	3	US-08-814-052-18	Sequence 18, Appl
14	200	6.3	2279	3	US-08-814-052-17	Sequence 17, Appl
15	198.5	6.2	1588	1	US-08-706-037-24	Sequence 24, Appl
16	198.5	6.2	1588	2	US-09-005-397-24	Sequence 24, Appl
17	198.5	6.2	1672	1	US-08-172-331B-13	Sequence 13, Appl
18	187.5	5.9	4403765	4	US-09-103-840A-2	Sequence 2, Appl
19	187.5	5.9	4411529	4	US-09-103-840A-1	Sequence 1, Appl
20	170.5	5.3	1722	4	US-09-221-275-3	Sequence 3, Appl
21	162.5	5.1	1176	3	US-08-669-421-18	Sequence 18, Appl
22	162.5	5.1	1176	4	US-09-389-528-18	Sequence 18, Appl
23	162.5	5.1	1176	4	US-09-181-827A-18	Sequence 18, Appl
24	162	5.1	3183	2	US-08-939-218A-1	Sequence 1, Appl
25	162	5.1	3192	1	US-08-940-661A-1	Sequence 1, Appl
26	162	5.1	3192	2	US-09-083-485-1	Sequence 1, Appl
27	157	4.9	2476	1	US-08-749-882A-1	Sequence 1, Appl
28	157	4.9	2476	2	US-08-539-134-1	Sequence 1, Appl
29	156.5	4.9	3192	1	US-08-706-037-26	Sequence 26, Appl
30	156.5	4.9	3192	2	US-09-005-397-26	Sequence 26, Appl
31	152	4.8	2476	5	PCT-US95-06816-1	Sequence 1, Appl
32	151.5	4.8	3187	5	PCT-US95-06815-1	Sequence 1, Appl
33	149.5	4.7	1170	3	US-08-689-421-20	Sequence 20, Appl
34	149.5	4.7	1170	4	US-09-389-528-20	Sequence 20, Appl
35	149.5	4.7	1170	4	US-09-181-827A-20	Sequence 20, Appl
36	132	4.1	1320	4	US-09-615-192A-207	Sequence 207, App
37	123.5	3.9	534	4	US-09-615-192A-254	Sequence 254, App
38	122.5	3.8	980	4	US-09-615-192A-208	Sequence 208, App
39	121.5	3.8	1161	3	US-08-689-421-22	Sequence 22, Appl
40	121.5	3.8	1161	4	US-09-389-528-22	Sequence 22, Appl
41	121.5	3.8	1161	4	US-09-181-827A-22	Sequence 22, Appl
42	121	3.8	2418	1	US-08-462-484-1	Sequence 1, Appl
43	121	3.8	2418	1	US-08-441-147-1	Sequence 1, Appl
44	121	3.8	2418	5	PCT-US95-07536-1	Sequence 118, App
45	113.5	3.6	538	4	US-09-615-192A-118	

ALIGNMENTS

RESULT 1
US-09-468-578-5
Sequence 5, Application US/09468578
Patent No. 639329
GENERAL INFORMATION:
APPLICANT: Wang, Huaming
APPLICANT: Bodie, Elizabeth A.
TITLE OF INVENTION: Phenol Oxidizing Enzymes
FILE REFERENCE: GC561-3
CURRENT APPLICATION NUMBER: US/09/468,578
CURRENT FILING DATE: 1999-12-21
PRIOR APPLICATION NUMBER: US 09/220,871
PRIOR FILING DATE: 1998-12-23
PRIOR APPLICATION NUMBER: US 09/338,723
PRIOR FILING DATE: 1999-06-23
NUMBER OF SEQ ID NOS: 17
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 5
LENGTH: 1791
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: CDNA
US-09-468-578-5
Alignment Scores:
Pred. No.: 0
Score: 3189.00
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
DB: 4
US-10-080-233-2 (1-594) x US-09-468-578-5 (1-1791)
OY 1 MetLeuPheLysSerTrpGlnLeuAlaAlaSerGlyLeuLeuSerGlyValLeuGly 20

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Db 7 ATGCTGTCAGATGCACTGACAGAGCCCTCGGAGCTCTGAGATCTCTCGC 66
QY 21 ILEPROMETASPTHGLYSERHISPROTLEGIUVALASPARGLVALYSTRGLU 40
Db 67 ATCCGAGTGGACCGGAGCCACCCATGAGGTGTGATCCGAGTAGAGTAGG 126
QY 41 VALPHEALASPSEULEUVALAALAGIYASAPASPTRGILSERPROTYR 60
Db 127 GTCCTCGCTGACCTCTGCTGCTGACAGGCGATGAGACTGGGAGTCCATC 186
QY 61 ASNLEULEUYRARGASNALAUEPROILEPPOVALYSGILPROLYSMETILE 80
Db 187 AACTGCTTACAGAAATGCCCTGCCAATCCACCTGCACAGCACCCCAAGTAT 246
QY 81 THRASNPROVALTHGLIYASAPILLETPTRYRGLIUEGILILEIISLEPHEGIN 100
Db 247 ACCAACCCTGTACCGGAGAGACATTTGGTACTATGAGATCGAATCAAGCATT 306
QY 101 GINARGILEYRPROTHLEUAPROALATHLEUVALGIYTYRASPGLYMETSER 120
Db 307 CAAGAGATTATCCACCTGGCCCTGCACTCGTGGGTACGATGAGTGAAGCCCT 366
QY 121 GLYPROTHRPHESNVALPROARGGLYTHRGILUTHRVALAARGPHEILEASNA 140
Db 367 GGTCTACTTTCAAAGTTCCAGAGAACAGAGACTGATGAGTTTCATCAACATGC 426
QY 141 THRVALGIUASERVALHISLEUHSISGLYSERPROSERARGALAPROPHASPL 160
Db 427 ACCGAGAGAACTGGGTTCATCTGCACGGCTCCCATGCGCTTCGATGTGG 486
QY 161 ALAELUASPVALTTHRPHESPROGLYGLUTRYLYSASPTRYRPHESASNTYGIN 180
Db 487 GCTGAAGATGACCTTCCCTGGCGAGTACAAAGATFACCTTCCCACTACCAATCC 546
QY 181 ALAARGLEULEUTRTRYHISASPHISALAPHEMETLSTHIALGIUASNALAYR 200
Db 547 GCCCGCTTCTGTGTACCATGACACCGCTTTCATGAAGACGCTGAGAAATCC 606
QY 201 GLYGINALAGIYALATYRILEILEASNASPGIUALAGIUSPALAUEGLYLEUP 220
Db 607 GGTGAGGCTGGGCGCTTACATTATACAGACGAGGCTGAGANGCTCTCGCTTCT 666
QY 221 GLYTYRGLYGLUPHESAPILEPROLEULEULEUTHRALALYSTYRTRYRASN 240
Db 667 GGTATGCGCGAGTTCGATATCCCTCTGATCCGAGGCGCAAGTACTATACCC 726
QY 241 THRLEUARGSERTHGLIYGLIUSPGLIUSPGLIUSPGLIUSPVALLIETHIS 260
Db 727 ACCCTGCGCTGACCGAGGAGGTGAGGACCAAGCCTGTGGGAGATGTATCCAT 786
QY 261 GLYGINPROTPRPHLEUASNAVALGINPROARGLYTYRARGPHEARGPHELE 280
Db 787 GGACAGCGCATGGCTTCTTACACTCCAGGCCCAAGTACCGTTCGATCTCTCA 846
QY 281 ALAALAVALSERARGALATRPHEULEUTRYRLEUVALARGTHRSESRPROAS 300
Db 847 GCTGCGGTCTCGGTGGCTGCTCTACTACCTCGTACAGACAGAGCTTCCCA 906
QY 301 ILEPROPHEGINVALILEALASERASPALAGIYLEULEGINALAPROVALGIN 320
Db 907 ATTCCTTTTCAAGTCAATGCTGTGATGCTGTGCTTCAAGCCCGCTCAGAC 966
QY 321 ASNLEUYRLEUVALAVALAGIUGARGTYRGLIUEILEIILEASPHETHRASN 340
Db 967 AACCTTACCTTGTGCTGTGGAGGCGATTACGAGATCATATTGACTTACCA 1026
QY 341 GLYGINTHRLEUASPLEUARGASNAVALAGIUTHRASNASPVAGIYASPOL 360
Db 1027 GGCCAGACTCTTGACCTCGCAGACGCTGCTGAGACCAAGATGTGCGGAGAG 1086
QY 361 TYRVALAARGTHRLEUGIUVALMETARGPHEVALVALSERSEGLYTHVALGI 380
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Db 1087 TACGCTCGCACTTCTCGAGGTGATGCGCTTGTGCTGACCTGCGACATGTTGAGACAAC 1146
QY 381 SERGINVALPROSETHRLEUARGSPVALPROPHESPROHISLYSGILPROLA 400
Db 1147 ACCGAGTCCCTTCACCTCTCCGATGCTTCTTCTCTTCCCTTCCACAGAGAGCCCCC 1206
QY 401 ASPLYRHSIPHELYSPHEGLIUNARGSERASNGIYRISTRYLEULILEASNAVAL 420
Db 1207 GACAGCACTTCAATTGAAACGAGCAAGAGACACTACGTGATCAACGATGTGGCTTT 1266
QY 421 ALASPVALASNGIUNARGVALLEUALALAYSPROGILUEGLYTHVALGIUVAL 440
Db 1267 GCCGATGTCAAGACGCTGCTCTGCGCAAGCCCGAGCTCGGACCGTTGAGCTGGAG 1326
QY 441 LEUGIUNASERSEGLIYTYRSEHISPROVALHISILEHISLEUVALASPHELY 460
Db 1327 CTCGGAACCTCTCTGGAGGCTGGAGCCACCCGCTCCACATTACCTTGTGACTTCAAG 1386
QY 461 ILEULEYRARGTHGLIYARGGLYGLIUNVALMETPROTYRGLIUSERALAGI 480
Db 1387 ATCTCAAGCGAACTGGTGTGCTGGCCAGGTCATGCTACGAGTCTGTGTCTAAG 1446
QY 481 ASPVALVALITRPLEUGLYARGGLYGLUTHRLEUTHRIEGLIUALHISTYRGLIN 500
Db 1447 GATGTCGTGTGGTGGGAGGGGTGAGACCTTGACCATCGAGGCCACTACCAACCTGG 1506
QY 501 THRGLIYALATYRMETTRPHISCYSHISASNEULEIILEHISGLIUSPASNA 520
Db 1507 ACTGAGCTTACATGTGGCAGCTGTCAACCTCATTCACGAGNARADAGACATGATGCT 1566
QY 521 VALPHEASNAVALTHRALAMETGLIUNLYSGIYTYRLEUGIUNASPHENGL 540
Db 1567 GATATCAAGCAGTCCCGCATGGAGGAGAAAGGATATCTTCAGAGACTTGGAGACCC 1626
QY 541 METASNPOLYSTTRARGALVALPROTYRASNAARGASAPHEHISALARGALAG 560
Db 1627 ATGAACCCCAAGTGGCGGCGCTTCTTACACACCCCAAGACTTCATGCTGCGCTGA 1686
QY 561 ASPHESERALAGUSERILETHRALARVALGINGLIUEUALAGIUGLNUPTRO 580
Db 1687 AACTTCTCGCGGAGATTCATACCTGCCGAGTGCAGAGTGGCCGACAGAGGCCGTAC 1746
QY 581 ASNARGLEUASPGIUILEUGIUNASPLEUGIYILEGLIUGLU 594
Db 1747 AACCGCTCGATGAGATCTGTGAGATCTTGGAAATCGAGAG 1788

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RESULT 2
 US-09-218-702-1
 ; Sequence 1, Application US/09218702
 ; Patent No. 6426410
 ; GENERAL INFORMATION:
 ; APPLICANT: Wang, Huang
 ; TITLE OF INVENTION: No. 6426410el Phenol Oxidizing Enzymes
 ; FILE REFERENCE: GC567
 ; CURRENT APPLICATION NUMBER: US/09/218,702
 ; CURRENT FILING DATE: 1998-12-22
 ; NUMBER OF SEQ ID NOS: 5
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 1
 ; LENGTH: 1791
 ; TYPE: DNA
 ; ORGANISM: Stachybotrys sp.
 US-09-218-702-1

Alignment Scores:
 Pred. No.: 0 Length: 1791
 Score: 3189.00 Matches: 594
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 100.00% Indels: 0
 DB: 4 Gaps: 0

US-10-080-233-2 (1-594) x US-09-218-702-1 (1-1791)

QY 1 MetLeuPheLysSerTrpGlnLeuAlaAlaSerGlyLeuSerGlyValLeuGly 20
 DB 7 ATGCTTTAAAGCATGGCACTGGCAGACGCTCCGGGCTCTGCTGGAGCTCTGGC 66
 QY 21 IleProMetAspThrGlySerHisProIleGluAlaValAspProGluValLysThrGlu 40
 DB 67 ATCCGATGGAGACCGGAGCCACCCCATTTGAGCGTTGATCCGAGATGAAGACTGAG 126
 QY 41 ValPheAlaAspSerLeuLeuAlaAlaGlyAspAspAspTrpGluSerProProTrp 60
 DB 127 GCTTCGTGACACCTCTCTGCTGCGAGAGGCGATGACGACCTGGAGTCACCTCATAC 186
 QY 61 AsnLeuLeuTrpArgGlnAlaLeuProIleProProValLysGlnProLysMetIleIle 80
 DB 187 AACTTCCTTTACAGGAATGCCCTGCCAATTTCCACTGTCAAGACCCCAAGATGATCAT 246
 QY 81 ThrAsnProValThrGlyLysAspIleTrpTrpTrpGluIleGluIleLysProPheGln 100
 DB 247 ACCAACCCCTGTACCCGCAAGGACATTTGTAATGATGATGATGATGATGATGATGAT 306
 QY 101 GlnArgIleLeuTrpThrLeuArgProAlaThrLeuValGlyTrpAspGlyMetSerPro 120
 DB 307 CAAGGATTTACCCCACTGGCCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 366
 QY 121 GlyProThrPheAsnValProArgGlyThrGluThrValValArgPheIleAsnAla 140
 DB 367 GGTCTCACTTCAATTTCCCAAGAGACAGACAGACTGATTAAGTTTCATCAACAATGCC 426
 QY 141 ThrValGluAsnSerValHisLeuHisGlySerProSerArgAlaProPheAspGlyTrp 160
 DB 427 ACCGTGAGAACCTGGTCCATCTGACGGCTCCCATCGGGTGGCTCCCTTTCATGGTGG 486
 QY 161 AlaGluAspValThrPheProGlyGlyTrpLysAspTrpTrpPheProAsnTrpGlnSer 180
 DB 487 GCTGAAGATGTACCTTCCCTGGCGAGTACCAAGATTTACTTCCCAACTCAATCCATCC 546
 QY 181 AlaArgLeuLeuTrpTrpHisAspHisAlaPheMetLysThrAlaGluAsnAlaTrpPhe 200
 DB 547 GCCCGCTCTCTGGTGGTACCATGACACCGCTTTCATCAAGACTGCTGAGATGCTCTTT 606
 QY 201 GlyGlnAlaGlyAlaTrpIleIleAsnAspGluAlaGluAspAlaLeuGlyLeuProSer 220
 DB 607 GGTCAAGCTGGCGCCATCAATTCATCAAGAGGCTGAGGATCTCTCGTCTCTCTAGT 666
 QY 221 GlyTrpGlyGluPheAspIleProLeuIleLeuThrAlaLysTrpTrpAsnAlaAspGly 240
 DB 667 GGTATGGCGAGTTCATATCCCTGTGATCTGACGGCCCAAGTACTATTAACGCCGATGGT 726
 QY 241 ThrLeuArgSerThrGluGlyGluAspGlnAspLeuTrpGlyAspValIleHisValAsn 260
 DB 727 ACCCTGCGTTCCGACGAGGTGAGGACGACGACTGTGGGAGATTCATTCATTCATTC 786
 QY 261 GlyGlnProTrpProPheLeuAsnValGlnProArgLysTrpArgPheArgPheLeuAsn 280
 DB 787 GGACAGCCATGGCTTCTCTTAACTGACGACCCCGCAAGTACCGTTCGATCTCTCAAC 846
 QY 281 AlaAlaValSerArgAlaTrpLeuLeuTrpLeuValArgThrSerProAsnValArg 300
 DB 847 GCTGCCGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 906
 QY 301 IleProPheGlnValIleAlaSerAspAlaGlyLeuLeuGlnAlaProValGlnTrpSer 320
 DB 907 ATTCCTTCCCAAGTCAATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 966
 QY 321 AsnLeuTrpLeuAlaValAlaGlyArgGlyIleIleIleAspPheThrAsnPheAla 340
 DB 967 AACCTCTACCTTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1026
 QY 341 GlyGlnThrLeuAspLeuArgAsnValAlaGluThrAspAspValGlyAspGluAspGlu 360
 DB 1027 GGCAGACTCTTGACTGCGCAACGTTGCTGAGACCAACGATGTGCGGAGGAGATGAG 1086

QY 361 TyrAlaArgThrLeuGluValMetArgPheValValSerSerGlyThrValGluAspAsn 380
 DB 1087 TAGCTTCGACACTCTCCAGGATGATGCCCTTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1146
 QY 381 SerGlnValProSerThrLeuArgAspValProPheProHisLysGluProAla 400
 DB 1147 AGCAGGTCCCTCCACTCTCCGTAAGCTTCTTCCCTCTCTCAAGAGAGCCCGCC 1206
 QY 401 AspLysHisPheLysPheGluArgSerAsnGlyHisTrpLeuIleAsnAspValGlyPhe 420
 DB 1207 GACAAACACTTCAAGTTTGAACGACCAACGACACTTACCTGATTCATCAACGATGGCTTT 1266
 QY 421 AlaAspValAsnGluArgValLeuAlaLysProGluLeuGlyThrValGluValTrpGlu 440
 DB 1267 GCCGATGTCAATAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1326
 QY 441 LeuGluAsnSerSerGlyGlyTrpSerHisProValHisIleHisLeuValAspPheLys 460
 DB 1327 CTCGAAACCTCTGAGAGCTGAGACCAACCCGCTCACATTCACCTTGTGTGACTTCAAG 1386
 QY 461 IleLeuLysArgThrGlyArgGlyGlnValMetProTrpGluSerAlaGlyLeuLys 480
 DB 1387 ATCTCAAGCAACTGTGGTGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGT 1446
 QY 481 AspValValTrpLeuGlyArgGlyGlyThrLeuThrIleGluAlaHisTrpGlnProTrp 500
 DB 1447 GATGTGCTGTGTTGGGAGAGGTTGAGACCTTCATCAAGAGCCCACTACCAACCTGG 1506
 QY 501 ThrGlyAlaTrpMetTrpHisCysHisAsnLeuIleHisGluAspAsnAspMetMetAla 520
 DB 1507 ACTGAGCTTACATGTGGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1566
 QY 521 ValPheAsnValThrAlaMetGluGlyLysGlyTrpLeuGlnLysAspPheGluAspPro 540
 DB 1567 GTATTCAGCTCACCCGCAAGGAGAGAGGATATCTTCAAGAGGACTTGCAGAGACCC 1626
 QY 541 MetAsnProLysTrpArgAlaValProTrpAsnArgAsnAspPheHisAlaArgAlaGly 560
 DB 1627 ATCAACCCCAAGTGGGCGCGCTTCTTCAACCGCAGACACTTCCATGCTCGCGCTGGA 1686
 QY 561 AsnPheSerAlaGluSerIleThrAlaArgValGlnGluLeuAlaGluGlnLysProTrp 580
 DB 1687 AACTTCTCCGCGAGTCCATCACTGCCGCGAGTGCAGAGTGCAGAGGAGCGGTAC 1746
 QY 581 AsnArgLeuAspGluIleLeuGluAspLeuGlyIleGlnGlu 594
 DB 1747 AACCGCTCGATGATGATCCCTGAGAGATCTTGGATGAGAG 1788

RESULT 3

US-09-218-702-5
 ; Sequence 5, Application us/09218702
 ; Patient No. 6426410

GENERAL INFORMATION:

; APPLICANT: Wang, Huaming
 ; TITLE OF INVENTION: No. 6426410el Phenol Oxidizing Enzymes
 ; FILE REFERENCE: GC567
 ; CURRENT APPLICATION NUMBER: US/09/218,702
 ; NUMBER OF SEQ ID NOS: 5
 ; SOFTWARE: FASTSEQ for Windows Version 4.0

SEQUENCE:

; SEQ ID NO 5
 ; LENGTH: 2067
 ; TYPE: DNA
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; OTHER INFORMATION: plasmid

US-09-218-702-5

Alignment Scores:

Pred. No.: 0
 Score: 3056.00
 Percent Similarity: 86.70%
 Best Local Similarity: 86.70%

Length: 2067
 Matches: 593
 Conservative: 0
 Mismatches: 1

Query Match: 95.83% Indels: 91
DB: 4 Gaps: 5
US-10-080-233-2 (1-594) x US-09-218-702-5 (1-2067)

QY 1 MetLeuPheLysSerTrpGluLeuAlaAlaSerGlyLeuLeuSerGlyValLeuGly 20
DB 10 ATGCTTCAAGTCAATGCAACTGGACAGCCCTGGGCTCTCTGGAGTCCCTGGC 69
QY 21 IleProMetAspThrGlySerHisProIleGluAlaValAspProGluValLysThrGlu 40
DB 70 ATCCGATGACACCGGACGCCACCCCATTTGAGCTGTGATCCCGAAGTGAAGACTAG 129
QY 41 ValPheAlaAspSerLeuLeuAlaAlaIaIaGlyAspAspTrpGluSerProTrp 60
DB 130 GTCTTCGCTGACTCCCTCTCTGCTGACAGCGGATGACGACTGGAGTCACTCCATAC 189
QY 61 AsnLeuLeu-----Tyr 64
DB 190 AACTTGCTTACAGGTGAGACACCTGCCACCTGTTTCCCTCGATTAACCTTAAT 249
QY 65 ArgAsnAlaLeuProIleProProValLysGlnProLysMet----- 78
DB 250 AGGAATGCCCTGCGCAATTCACCTGTCAAGCAGCCCAAGATGTATGCTTGATTTCTA 309
QY 79 -----IleIleThrAsnProValThrGly 87
DB 310 CGAAGCACTCGGCCCGCACTAATGTATTTCTAGATCAATTACCAACCTGTCCAGGCA 369
QY 87 SASPILeTrpTyrTyrGluIleGluIleLysProPheGlnIaArg----- 102
DB 370 GGACATTTGGTACTAGATGAGATCGAGATCAAGCCATTTCAAGAGGTGAGTTGCTCAG 429
QY 103 -----IleTyrProThrLeuAspPr 109
DB 430 AAACCTTGCGTAATTAATCATGTTACTGACCCCTTTCAGATTACCCACCTTGCGCC 489
QY 109 oAlaThrLeuValGlyTyrAspGlyMetSerProGlyProThrPheAsnValProArg 129
DB 490 TGGCAGCTCGTCGCGCTAGATGGATGAGCCCTGCTCTCAATGTTCCAGAGG 549
QY 129 YThrGluThrValValaArgPheIleAsnAsnAlaThrValGluAsnSerValHisLeu 149
DB 550 AACGAGACTAGTACTGATTCATCAACAAATGCCCTGGGAACTGGTCCATCTCA 609
QY 149 SGISeProSerAlaGlaProPheAspGlyTrpAlaGluAspValThrPheProGly 169
DB 610 CGGCTCCCATCGCGTCCCTTTCGATGTTGGCTGAGATGTGACCTTCCGCGCA 669
QY 169 uTyrLysAspTyrTyrPheProAsnTyrGlnSerAlaArgLeuLeuTrpTyrHisAsp 189
DB 670 GTACAAGATTAATCACTTCCCACTACCAATCCGCCCTCTGTGTGACCAAGACA 729
QY 189 sAlaPheMetLys----- 193
DB 730 CGCTTTCATGAA-GGTATGCTACGAGCCCTTATCTTCTTGCTGCTTGGCTAACCA 788
QY 194 -----ThrAlaGluAsnAlaTyrPheGlyGlnAlaGlyAlaTyrIleLeu 209
DB 789 CTTCCTTTCGATGACTGCTGAGAAATGCTTACTTGTGTAGGCTGGCGCTCAATATATA 848
QY 209 nAspGluAlaGluAspAlaLeuGlyLeuProSerGlyTyrGlyGluPheAspIlePro 229
DB 849 CGAGAGAGCTGAGATGCTCGCTCTCTAGTGGCTATGGCGAGTTCCGATATCCCTCT 908
QY 229 uIleLeuThrAlaLysTyrTyrAsnAlaAspGlyThrLeuArgSerThrGluGlyAla 249
DB 909 GATCTGAGCGCAAGTACTATAACCGGATGTAACTCGCTTCGACCGAGGAGTGAAGA 968
QY 249 pGluAspLeuTrpGlyAspValIleHisValAsnGlyGlnProTrpProPheLeuAsp 269
DB 969 CCAGGACCTGTGGGAGATGATCATCATGTCATCAAGGAGACGACGCTTTCCTTAACGT 1028

QY 269 IGlnProArgLysTyrArgPheArgPheLeuAsnAlaAlaValSerArgAlaTrpLeu 289
DB 1029 CCAGCCCGGCAAGTACCGCTTTCGATTCCTCAAGCTCCGCTGCTGCTGCTCTCT 1088
QY 289 uTyrLeuValArgThrSerSerProAsnValArgIleProPheGlnValIleAlaSer 309
DB 1089 CTACCTCGTCAGGACACTCTCCCACTGAGAAATTCCTTCCAAAGTCAATGCTCTGCA 1148
QY 309 pAlaGlyLeuLeuGlnAlaProValGlnThrSerAsnLeuTyrLeuAlaValAlaGlu 329
DB 1149 TCTGTCTCTCAAGCCCGGTTCAAGACCTTAACCTTAACCTTGTGTTGGCGAGCG 1208
QY 329 GTYrGluIleIleIle----- 334
DB 1209 TTACAGATTCATTTATGTTATGCTCCCTCCCTCCATGCAATGATGCAAGACTTAAGCT 1268
QY 335 -----AspPheThrAsnPheAlaGlyGlnThrLeuAspLeuArgAsnValAlaG 351
DB 1269 AACACTGTAGACTCACCAACTTTCGCGCAGACTTTCGACCTGCGCAAGCTTGCTGA 1328
QY 351 uThrAsnAspValGlyAspGluAspGluTyrAlaArgThrLeuGluValMetArgPhe 371
DB 1329 GACCAAGATGTGCGCGAGAGATGATGACTGCTGCACTCTCGAGGTATGCGCTTCT 1388
QY 371 IValSerSerGlyThrValGluAspAsnSerGlnValProSerThrLeuArgAspVal 391
DB 1389 CGTCAGCTCTGGCACTGTGAGGACACAGCAGAGTCCCTCCCACTCTCCGAGAGTTCC 1448
QY 391 OPheProTrpHisLysGluGlyProAlaAspLysHisPheLysPheGluArgSerArg 411
DB 1449 TTTCCCTCTCAAGAGAGGCCCGCGAGAACACTTCAAGTTGAACACGACGACAGG 1508
QY 411 YHisTyrLeuIleAsnAspValGlyPheAlaAspValAsnGluArgValIleAlaLys 431
DB 1509 ACACACTGTGATCAACGATGTGCTTGGCTTCCGATGTCAATGAGCTGTCTGCGCAAGC 1568
QY 431 oGluLeuGlyThrValGluValTrpGluLeuGluAsnSerSerGlyTyrPheHisPr 451
DB 1569 CGAGCTCGGCAACCGTTGAGGTCTGGAGCTCGAGAACTCTCTGGAGGCTGAGCACACC 1628
QY 451 oValHisIleHisLeuValAspPheLysIleLeuLysArgThrGlyArgGlyGlnVal 471
DB 1629 CGTCCACATTCACCTTGTGACTTCACATCTCAAGGAACTGCTGCTGCGCAAGT 1688
QY 471 IMeProTyrGlnSerAlaGlyLeuLysAspValValTrpLeuGlyArgGlyGluThr 491
DB 1689 CATGCCCTACAGATCTGCTGCTTAAAGATGCTCTGCTGTTGGGCAAGGGTGAACCT 1748
QY 491 uThrIleGluAlaHisTyrGlnProTyrTrpThrGlyAlaTyrMetTrpHisCysHisAsn 511
DB 1749 GACCATCGAGGCCCTACCAACCTGGAGCTGAGACTTAACATGTGACACTGTCAACACT 1808
QY 511 uIleHisGluAspAsnAspMetMetAlaValPheAsnValThrAlaMetGluGluGly 531
DB 1809 CATTCAAGAGATTAACGATGATGCTGATTTCAACCTCACCGCCAGGAGGAGAAAGG 1868
QY 531 YTyrLeuGlnGluAspPheGluAspProMetAsnProLysTrpAlaValProTyrAs 551
DB 1869 ATATCTTAGAGAGACTTCGAGGACCCCATTAACCCCAAGTGGCGGCTTCTTACAA 1928
QY 551 nArgAsnAspPheHisAlaArgAlaGlyAsnPheSerAlaGluSerIleThrAlaArg 571
DB 1929 CCGCAAGCACTTCATGCTCGCGTGGAACTTCTCCCGAGTCCATCACTGCGCGAGT 1988
QY 571 IGlnGluLeuAlaGluGlnGluProTyrAsnArgLeuAspGluIleLeuGluAspLeu 591
DB 1989 GCAGGAGTGGCCAGGAGGAGCGGTCAACCGCTGATAGATCTCGAGGATCTTGG 2048
QY 591 YIleGluGlu 594
DB 2049 AATCGAGAG 2058

RESULT 4

US-09-468-578-1
; Sequence 1, Application US/09468578
; Patent No. 6393329
; GENERAL INFORMATION:
; APPLICANT: Wang, Huaming
; APPLICANT: Bodie, Elizabeth A.
; TITLE OF INVENTION: Phenol oxidizing Enzymes
; FILE REFERENCE: GC561-3
; CURRENT APPLICATION NUMBER: US/09/468,578
; PRIORITY FILING DATE: 1999-12-21
; PRIORITY FILING DATE: 1998-12-23
; PRIORITY FILING DATE: 1998-12-23
; PRIORITY FILING DATE: 1999-06-23
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 3677
; TYPE: DNA
; ORGANISM: Stachybotrys chartarum
09-468-578-1

Alignment Scores:
Pred. No.: 0 Length: 3677
Score: 3056.00 Matches: 593
Percent Similarity: 86.70% Conservative: 0
Best Local Similarity: 86.70% Mismatches: 1
Query Match: 95.83% Indels: 91
DB: 4 Gaps: 5

US-10-080-233-2 (1-594) x US-09-468-578-1 (1-3677)

QY 1 MetLeuPheLysSerTrpGlnLeuAlaAlaSerGlyLeuSerGlyValLeuGly 20
DB 1044 ATGCTTTAGAGTACGACGACGACGACGACGCTCCGGCTCTGTGAGTCTCGGC 1103
QY 21 IleProMetAspThrGlySerHisProIleGluAlaValAspProGluValIleThrGlu 40
DB 1104 ATCCCGATGGACACCGGACGCCACCCATTGAGGCTGTGATCCCGAAGTGAAGACTGAG 1163
QY 41 ValPheAlaAspSerLeuLeuAlaAlaIleGlyAspAspAspTrpGluSerProProTyr 60
DB 1164 GCTTCGTGACCTCCCTCTGCTGACGAGGAGGATGACGACGAGTCCATAC 1223
QY 61 AsnLeuLeu-----Tyr 64
DB 1224 AACTCTCTTACAGGTGAGACACCTCTCCACCTGTTCCTCCGATTAACCTCTTAT 1283
QY 65 ArgAsnAlaLeuProIleProValIleGlnProLysMet----- 78
DB 1284 AGGAATGCCCTGCCAATTCACCTGTCAGACGCCCAAGATGTATGCTTGTATTTCTA 1343
QY 79 -----IleIleThrAsnProValIleThrGly 87
DB 1344 CGAAGCACTCGGCCCGACCTATGTATTTAGAGCACTTACCAACCTGTGCAACGCGCAA 1403
QY 87 SasPIleTrpTyrTrpGluIleGluIleLysProPheGlnGlnArg----- 102
DB 1404 GGACATTTGTACTATGAGATGAGATCAAGCCATTTCAGCAAGAGGTGAGTTGCTCAG 1463
QY 103 -----IleTyrProThrLeuArgPr 109
DB 1464 AAACCTGTGTAATTAATCATCTTACTGACCCCTTTCAGATTTCACCCACTTGGCGCC 1523
QY 109 OAlaThrLeuValGlyTyrAspGlyMetSerProGlyProThrPheAsnValProArgGly 129
DB 1524 TTCACACTCTCGCTGCTGATGATGAGATGAGCCCTGCTCTACTTCAATGTTCCAGAG 1583
QY 129 YThrGlnThrValIleArgPheIleAsnAsnAlaTrpValIleGluAsnSerValHisLeuH 149
DB 1584 AACAGAGACTGTAGTGTAGTCAATCAACATGCGACCGTGGAGAACTCGGTCATGTGGA 1643
QY 149 sGlySerProSerArgAlaProPheAspGlyTrpAlaGluAspValThrPheProGlyGly 169

DB 1644 CGGCTCCCAACWCCGCTGCCCTTCATGTGTGGGCTGAAGATGTGACCTTCCCTGACGA 1703
QY 169 uTyrLysAspTyrTrpPheProAsnTyrGlnSerAlaArgLeuLeuTrpTyrHisAspH 189
DB 1704 GTACCAAGATTAATCTTCCCAATCAATCCCGGCTTCTGTGTACATGACCA 1763
QY 189 sAlaPheMetLys----- 193
DB 1764 CGCTTTCATCAAC-GGATAGCTACGAGCCTTATCTTGTGGCTACCTTGGCTAACCA 1822
QY 194 -----ThrAlaGluAsnAlaTyrPheGlyGlnAlaGlyAlaTyrIleLeas 209
DB 1823 CTTCCTTGTGATACGCTGAGATGCTGCTTGTGACAGCTGGCGCTTACATTAACAA 1882
QY 209 nAspGluAlaGluAspAlaLeuLysLeuProSerGlyTyrGlyGluPheAspIleProLe 229
DB 1883 CGACGAGGCTGAGAGATGCTCTGCTCTTCTAGTGGCTATGGAGATGATATCCCTCT 1942
QY 229 uIleLeuThrAlaLysTyrTrpAsnAlaAspGlyThrLeuArgSerThrGluGluAs 249
DB 1943 GATCTGACGCGCCCAAGTACTATTAACGCCGATGCTGCTGCTTCCACCGAGGTGAGGA 2002
QY 249 pGlnAspLeuTrpGlyAspValIleHisValAsnGlyGlnProTrpProPheLeuAsnVa 269
DB 2003 CCAGAGACCTGTGGGAGATGCTATTCATGCAACGAGCAGCAGCATGGCTTCTTAACGT 2062
QY 269 LglnProArgLysTyrArgPheArgPheLeuAsnAlaAlaValSerArgAlaIlePheLe 289
DB 2063 CCAGCCCGCAACATACCGTTCGATTCCTCAACGCGCTGCTGCTGCTGCTGCTGCT 2122
QY 289 uTyrLeuValArgThrSerSerProAsnValArgIleProPheGlnValIleAlaSerAs 309
DB 2123 CTACCTCTGTAGAGACCAAGCTCTCCCAACGTCAGAAATTCCTTCCAACTCTTGCCTCTGA 2182
QY 309 pAlaGlyLeuLeuGlnAlaProValGlnThrSerAsnLeuTyrLeuAlaValAlaGluArg 329
DB 2183 TGCTGGCTCTCTCAAGCCCGCTGACAGCTCTTAACCTTACTGCTGTGCGGAGCG 2242
QY 329 gTyrGluIleIleIle----- 334
DB 2243 TTACGAGATCATTAATTTGATGATGCTCCCTCCCTCCACGAATGACTCAAGAACTTAACACT 2302
QY 335 -----AspPheThrAsnPheAlaGlyGlnThrLeuAspLeuArgAsnValAlaGly 351
DB 2303 AACACTGTGTAGATTTCAACCACTTGTGCTGCGACGCTTGACTGCGCAACGTGTGTA 2362
QY 351 uThrAsnAspValGlyAspGlyAspGlyLysTrpAlaArgThrLeuGluValMetArgPheVa 371
DB 2363 GACCAACGATGTGCGGACGAGATGATGATGCTGCGACTCTCGAGGTGATGGCGTTGCT 2422
QY 371 ValSerSerGlyThrValGluAspAsnSerGlnValProSerThrLeuArgAspValPr 391
DB 2423 CGTCACCTCTGCGACCTGTGTAGGACAAACACCGCTCCCTCCACTCTCGTCAACGTTCC 2482
QY 391 oPheProProHisLysGlnGlyProAlaAspLysHisPheLysPheGluArgSerAsnGly 411
DB 2483 TTTCCTCTCTCAAGAGAGAGGCGCGCGCAAGACCTTAAGTTGAAACGAGCAACGG 2542
QY 411 yHisTyrLeuIleAsnAspValGlyPheAlaAspValAsnGluArgValLeuAlaLysPr 431
DB 2543 ACACCTACCTGATCAACAGATGTGCTTGGCGATGTCAATGACGCTGTCTGCGCAAGCC 2602
QY 431 oGluLeuGlyThrValGluValTrpGluLeuGluAsnSerSerGlyGlyTrpSerHisPr 451
DB 2603 CGAGCTCGGACACCTGTGAGGTGCGAGGCTCGAAGAACTCTGTGAGAGGTGAGCAACCC 2662
QY 451 oValHisIleHisLeuValAspPheLysIleLeuLysArgThrGlyArgGlyGluVal 471
DB 2663 CGTCCACATTCACCTTGTGACTTCAAGATCTCAAGCGAACTGTGTGTGCTGCGCAAGGT 2722
QY 471 lMetProTyrGluSerAlaGlyLeuLysAspValValTrpLeuGlyArgGlyGlyLysThrLe 491

QY 371 lvalserSerglyThrValGluaspasnsrGlnValProSerThrleuArgaspValPr 391
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Db 2423 CGTCACTCTGGACACTGTGGAGACAACACCGGTCCTCCACTCTCCGTACGTTCC 2482
QY 391 opheProProHISLysGluGlyProAlaaspLysHISpHelysPheGluuArgSeransG 411
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Db 2483 TTTCCTCTCCACAAAGAAAGGCCCGCCGACCAAGCACTTCAAGTTGAAAGCGAACAAAG 2542
QY 411 yHISThrleuLeuaspValGlyPheAlaaspValaspGluuArgValLeuAlaLysPr 431
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Db 2543 ACCTACCTGATCAACGATGTTGGCTTGGCATGTCATGACCGTCTCCGACCAAGCC 2602
QY 431 ogLueGlyThrValGluValTrpGluLeuGluaspSerSerglyGlyTrpSerHISPr 451
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Db 2603 CGAGCTCGGACACCGCTTGAGGTCTGGAGAGCTCGAAGACTCTCTGGAGCTGGAGCCACC 2662
QY 451 oValHISLISLISLISLISLISLISLISLISLISLISLISLISLISLISLISLISLIS 471
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Db 2663 CGTCCACATTCACCTGTTGACTTCAAGATCCCAAGCGAAGCTGGTGGCCAGGT 2722
QY 471 lMetProGlyGluSerAlaGlyLeuLysaspValValTrpLeuGlyArgGlyLysLys 491
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Db 2723 CATGCCCTACGAGTCTGGCTGTCTTAAGATGCTGTGGTGGAGGGGTAGACCTT 2782
QY 491 uThrIleGluAlaHISLISLISLISLISLISLISLISLISLISLISLISLISLISLIS 511
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Db 2783 GACCATCGAGGCCCATACCAACCCGAGCTGAGCTTACATGTGGCAGCTGTACAACT 2842
QY 511 uLISLISLISLISLISLISLISLISLISLISLISLISLISLISLISLISLISLIS 531
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Db 2843 CATTCACGAGGATTAACGACATGATGCTGATTCACAGCTCACCGCATGAGAGAAAGG 2902
QY 531 yThrLeuGlnGluaspPheGluaspProMetaspProLysTrpArgAlaValProTyras 551
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Db 2903 ATATCTTCAGAGGACTCTGGAGGACCCCATGAACCCCAATGGCGCTCTCTTACAA 2962
QY 551 nArgaspAspPheHISLISLISLISLISLISLISLISLISLISLISLISLISLISLIS 571
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Db 2963 CGGCAACGACTTCATGCTCGGCTGGAACCTCTCGCGAGCTCATCTCCCGAGT 3022
QY 571 lGlnGluLeuAlaGluGlnGluProTyraspArgLeuaspGluIleLeuGluaspLeuG 591
|||||
Db 3023 GCAGGAGCTGGCGGACAGAGCCCTCAACCCCTCGATGAGATCTCTGGAGATCTTGG 3082
QY 591 yIleGluGlu 594
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Db 3083 AATCGAGAG 3092

ULT 6
09-468-578-6
Sequence 6, Application US/09468578
Patent No. 6,300,329

GENERAL INFORMATION:
APPLICANT: Wang, Huang
APPLICANT: Bodie, Elizabeth A.
TITLE OF INVENTION: Phenol Oxidizing Enzymes
FILE REFERENCE: GC561-3
CURRENT APPLICATION NUMBER: US/09/468, 578
CURRENT FILING DATE: 1999-12-21
PRIOR APPLICATION NUMBER: US 09/220, 871
PRIOR FILING DATE: 1998-12-23
PRIOR APPLICATION NUMBER: US 09/338, 723
PRIOR FILING DATE: 1999-06-23
NUMBER OF SEQ ID NOS: 17
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 6
LENGTH: 2063
TYPE: DNA
ORGANISM: Curvularia pallescens
US-09-468-578-6

Alignment Scores: 1.05e-201 Length: 2063
Pred. No.:

Score: 1870.00 Matches: 365
Percent Similarity: 67.62% Conservative: 82
Best Local Similarity: 55.22% Mismatches: 133
Query Match: 58.64% Indels: 82
DB: 4 Gaps: 11

US-10-080-233-2 (1-594) x US-09-468-578-6 (1-2063)

QY 2 LeuPheLysSerTrpGlnLeuAlaAlaSerGlyLeuLeuSerGlyValLeuGlyTle 21
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Db 16 CTCTCTCCGCACTTCACTCGCTTCA-----ATTCCGAAGGCAATATACGGGCTT 66
QY 22 ProMetaspPheGlySerHISProIleGluAlaValaspProGluValLysThrGluVal 41
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Db 67 GCTTTG-----AGCGAGCTCTCTGCCAAATATATITACGAACACCCCGACGAAGAAAG 120
QY 42 PheAlaaspSerLeuAlaAlaAlaGlyasp----- 53
|||||
Db 121 GCTGCC-----CTGGCAGCCATCGTTGAAGATGACCCCTGCCATGTTTCAGATTCCTG 174
QY 54 ---AspTrpGluSerProProTyraspLeuLeuTyrArgaspAlaLeuProIleProPro 72
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Db 175 AAGGACTGGCAAGAGCCCGAGATATCCCATCTTTTTCGAGGACACTGCCATTCCTTCCA 234
QY 73 ValLysGlnProLys----- 77
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Db 235 GCCAAGAACCGAAGTAGTACGTTGATTCATGACATGACAGCTTCTTACAAATATGCTCA 294
QY 78 -----MetIleIleThrAspProValThrGlyLysaspIleTrpTyrGlyIle 94
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Db 295 CCCATCCGAGTAAATATGACGAATCTCTGACAAACAAAGAGATCTGTACTAGAGAT 354
QY 95 GluIleLysProPheGlnGlnArgGlyIleTyrProThrLeuArgProAlaThrLeuValGly 114
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Db 355 GTCATCAAAACCTTTTAAACCAAGCTTATCCAGTCTGCTGCTGCTGCTGCTGCTGCTG 414
QY 115 TyrAspGlyMetSerProGlyProThrPheaspValProArgGlyThrGluThrVal 134
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Db 415 TATGATGCGCATTTTACCAGGCTCTACGATATGCTGCGGAGAGAACAGAACGCCGTTGTA 474
QY 135 ArgPheIleaspAspAlaThrValGluaspSerValHISLISLISLISLISLISLISLIS 154
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Db 475 CGATTCGTAACACAGGCTGATCCGAGAGTTCATTCATTCATTCATTCATTCATTCATTC 534
QY 155 AlaProPheaspGlyTrpAlaGluaspValThrPheProLys----- 168
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Db 535 GCCCCTTTGACGATGGCTGAAGATTTGAT-TATGAAAGGCCAATTCAAAGGTACAC 593
QY 169 -----GluTyrLysaspTyr 173
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Db 594 AGAACAATCTTATGATCATGAGGTCCTTTTATACACAGACTGCTTCTTAGACTTAC 653
QY 174 TyrPheProaspNTrpGlnSerAlaArgLeuLeuTrpTyrHISaspHISala----- 190
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Db 654 TACTACCCGAACAACAGGCTGCCAGATCTCTGTAACACATCATGCTATGATGATGT 713
QY 191 -----PheMetLys 193
|||||
Db 714 GTAAGCTTCGACACTAATCATGAGCGAAGCAAGATCGGGCTGACACTTATGACAG 773
QY 194 ThrAlaGluaspAlaTyrPheGlyAlaAlaGlyAlaTyrIleIleaspGluAlaGlu 213
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Db 774 ACTGCGGAATAATCCCTTATTTTGGACAGGCTGGGCTCTACGTATCACAGCCACAGCTGAG 833
QY 214 AspAlaLeuGlyLeuProSerGlyTyrGlyGluPheaspIleProLeuIleLeuThrAla 233
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Db 834 GACGCCCTCGGCTTCTCTGCGGTACGAAATACAGATCCACATGCGGTCTCAGTTC 893
QY 234 LysTyrTyrAspAlaaspGlyThrLeuArgSerThrGluGlyLysaspGlnaspLeuTrp 253
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Db 894 AAGTCTTACAAACAGTATGTAACCTTCCACAGAGTGGAGAACGAACAACTCTCTGG 953
QY 254 GlyaspValIleHISLISLISLISLISLISLISLISLISLISLISLISLISLISLISLISLIS 273

Db 706 AGCGTGTGATTCACGATCAGAAAGCCCTCATCTAATCAAGACCTTCCTCTCAGAC 765
Qy 173 TTTTphheproasnTyrgInserAlaArgLeuThrPrpYrHisAspHisAlaPhe-Me 192
Db 766 TACTACTACCCGAAACCAAGAGTCGAGATTTTGTGTACACGATCATGATGATCAT 825
Qy 192 T----- 192
Db 826 GTTGTAGTCTTACCGACCTTTCATGTAGTGAAGGAAGATTAAGCTACATCTGT 885
Qy 193 -LysThrAlaGluAsnAlaTyrrPheGlyGlnAlaGlyAlaTyrrIleIleAsnAspGluAl 212
Db 886 GCAGACCCGCAAAATGCTATTTCCGGCAAGCCGGCCCTACCTGTATCAAGACCCGGC 945
Qy 212 AGIAspAlaLeuGlyLeuProSerGlyTyrrGlyGlnPheAspIleProIleLeuTh 232
Db 946 TGAAGATGCTCTGGCCCTTCCTTCAGGTTCAGGAAATACACACTTCGGCTGCTCAG 1005
Qy 232 TAlaLysTyrrAsnAlaAspGlyThrLeuArgSerThrGlyGlnAspGlnAspLe 252
Db 1006 TTCCAAGTACTACAGCCGATGGAAGTCTTAAGACACAGTGTGGAGAACAGACAGTGT 1065
Qy 252 UTTPGlyAspValIleHisValasnGlyGlnProTrpProPheLeuAsnValGlnProAr 272
Db 1066 TTGGGGCGACATCATCATGTCAAAGCGTCAAGCCCTGGCCATTTCTTAATGTGAGCCTCG 1125
Qy 272 GlyTyrrArgPheArgPheLeuAsnAlaAlaValSerArgAlaTrpLeuLeuTyrrLeuVa 292
Db 1126 AAGATATCGTCTTCGATTCCTCAACGGCGCTTTCAGAACTTCCCTTCCTTCCTGT 1185
Qy 292 LArgThrSerProAsnValArgIleProPheGlnValIleIleAsnAspAlaGlyLe 312
Db 1186 CAAGCAAGAACACACTGCCACTAGCTTCCTTCCTTCAGTCACTTCCTGTATGAGAGGCT 1245
Qy 312 ULeuGlnAlaProValGlnThrSerAsnLeuTyrrLeuAlaValAlaGluArgTyrrGlu 332
Db 1246 ACTCACACACCCGTTCAACCTCAGATATGTATGTATGTAGCCGCAAGACGCTACGAGAT 1305
Qy 332 eIleIleAspPheThrAsnPheAlaGlyGlnThrLeuAsnLeuArgAsnValAlaGluTh 352
Db 1306 TGTGTTGATTTGGCCGCTTCATGCCGCAAAAGCTTGATCTGGCAACTTCGCAAAAGC 1365
Qy 352 rAsnAspValAlaGlyAspGluTyrrAlaArgThrLeuGlnValAlaMetArgPheValVa 372
Db 1366 CAAATGATATGATACGACGACGACGACGACGACGACGACGACGACGACGACGACGACG 1425
Qy 372 lSerSerGlyThrValGluAsnAsnSerGlnValProSerThrLeuArgAspValProPh 392
Db 1426 CACAGGCAAAAGCTCGTCACTGATCACTCGTGTGACCGACGACGACGACGACGACGACG 1485
Qy 392 ePrProHisLysGluGlyProAlaAspLysHisPheLysPheGluArgSerArgGlyH 412
Db 1486 CCGCGCGGACAAAGCC--GACATAGAACATCACTTCGTTCCATGCTCAACAAAGCGCA 1542
Qy 412 sTyrrLeuIleAsnAspValGlyPheAlaAspValAsnGluArgValLeuAlaLysProG 432
Db 1543 GTGGCGCATCAAGCGGATCGGGTTTGACAGCTGGAACGCGTGTTCGCAAGAGTACC 1602
Qy 432 ULeuGlyThrValGluValTrpGluLeuGluAsnSerSerGlyGlyTrpSerHisProVa 452
Db 1603 GCAGCGTACGTCTGAGCTTTGGGAACTTGAGAACGCTCGCGCGCTGCTACACCCCAT 1662
Qy 452 lHisIleHisLeuValAspPheLysIleLeuLysArgThrGlyGlyArgGlyGln----- 470
Db 1663 CCAAGTCCACCTGTAAGTCTTCGAGTGTGCGACGCTACGCGGACGACGACGACGACGCTCCGG 1722
Qy 471 -ValMetProTyrrGluSerAlaGlyLeuLysAspValAlaTrpLeuGlyArgGlyGluTh 490
Db 1723 CGTCATGCCCTATAGAGCGCGCGCTTCAGAGAGCTGTGTGGCTGCGCGCTCAGAGAC 1782
Qy 490 rLeuThrIleGluAlaHisTyrrGlnProTrpThrGlyAlaTyrrMetTrpHisLysHis 510
Db 1783 GGTCTCTGTCGAAGACATTACGCGCCATGAGAGGAGTCTACATGTTCCACACTGCCAAG 1842

Qy 510 nLeuIleHisGluAspAsnAspMetMetAlaValPheAsnValThrAlaMetGluGly 530
Db 1843 CTTATCTCAGCAAGACCAAGCATGATGCGCTTCGACTGTACTAACTCCGAACCTT 1902
Qy 530 sGlyTyrrLeuGln--GluAspPheGluAspProMetAsnProLysTrpArgAlaValPr 549
Db 1903 TGGGTACACAGACAGCACTGATTTCCAGATCTGAGAGATCTCGCTGGTGCAGACAGC 1962
Qy 549 cTyrrAsnArgAsnAspPheHisAlaAlaGlyAlaAsnPheSerAlaGluSerIleThrAl 569
Db 1963 TTTCACCGCGGGTATCTCAACGCGCATCGGTATCTTTTCACAGAAATCCATCAGAGCC 2022
Qy 569 aArgValGlnGluLeuAlaGluGlnGluProTyrrAsnArgLeuAspGluIleLeuGluAs 589
Db 2023 TAGATTAATGATGTGGGCTCGACAGCCCTTACAGCAAGCTCCACAAATTACAGCCTC 2082
Qy 589 pLeu 590
Db 2083 GCTC 2086

RESULT 8
US-09-401-476-1
Sequence 1, Application US/09401476
Patent No. 6168936
GENERAL INFORMATION:
APPLICANT: Wang, Huaming
TITLE OF INVENTION: No. 6168936el Phenol Oxidizing Enzymes
FILE REFERENCE: GC584
CURRENT APPLICATION NUMBER: US/09/401.476
CURRENT FILING DATE: 1999-09-22
NUMBER OF SEQ ID NOS: 8
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 1
LENGTH: 1958
TYPE: DNA
ORGANISM: Stachybotrys chararum
US-09-401-476-1

Alignment Scores:
Pred. No.: 1.75e-173 Length: 1958
Score: 1620.50 Matches: 331
Percent Similarity: 65.89% Conservative: 67
Best Local Similarity: 54.80% Mismatches: 125
Query Match: 50.82% Indels: 83
Gaps: 11

US-10-080-233-2 (1-594) x US-09-401-476-1 (1-1958)

Qy 57 SerProProTyrrAsnLeuLeuTyrrArgAsnAlaLeuProIleProProValLysGlnPro 76
Db 145 AGTCTCTCCCTG--GCCTTGTACGAAGTGCCTCTCGGATCCCTCTGAAGCGGCC 201
Qy 77 Lys-----Met-Ile11 80
Db 202 AAGTAAGTAAGTACATTCTATAGCGCTAGACAGCAAGCTTGCTAATCATTCGCAATACCGT 261
Qy 80 eThrAsnProValThrGlyLysAspIleTrpTyrrGlyIleGluIleLysProPheG 100
Db 262 CCCCACCCCAACCACTGAGAGGACATCTGTACTACAGATGAGATTAAGGCCCTCTC 321
Qy 100 nGlnArgIleTyrrProThrLeuArgProAlaThrLeuValGlyTyrrAspGlyMetSerPr 120
Db 322 CCACCAATATCTACCTTATCTGAGCGCGGCAACATGTTGGATGATGATGATGATGATGATG 381
Qy 120 oGlyProThrPheAsnValProArgGlyThrGluThrValAlaArgPheIleAsnAla 140
Db 382 AGAGCATACATCATCTCTCTCTCTGTCGACATGAGATGTGTCTCGTTCGGAACAGCGG 441
Qy 140 a-----ThrValGluAsnSerValHisLeuHisGlySerProSerArgAlaProPheAs 158
Db 442 AGAGACACCTTCCTCCCAACAGCGCTGACAGCGCTTCTCTGAGCTCCTTGA 501

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QY 158 pGlyTPAlaGluAspValThrPheProGlyGluTyrLysAspTyrPheProAsnTyr 178
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QY 178 rGlnSerAlaArgLeuLeuTyrPheHisAspHisAlaPheMetLysThrAlaGluAsnAl 198
Db 562 GCAGGCTCCCGCAGCTTTGGTGTACATGACCATCCATGTCATCACCAGCCGAGAACGC 621
QY 198 aTyrPheGlyAlaGlyAlaTyrIleIleAsnAspGluAlaGluAspAlaLeuGlyLe 218
Db 622 CTACATGGGTGAGGCTGGTGTCTACATGATCCAGACCCGCTGAGATGCCCTTAACCT 681
QY 218 uProSerGlyTyrGlyGluPheAspIleProLeuIleLeuThrAlaLysTyrTyrAsnAl 238
Db 682 CCCCAGCGCTACAGCGCGAGTTGATATCCCTTGGTGTGACTGCGCAAGCGATACAGCG 741
QY 238 aAspGlyThrLeuAspSerThrGluGlyGluAspGlnAspLeuThrPglAspValIle- 257
Db 742 AGACGGCACTCTCTCTCCACCAATGAGAGGTTCCAGCTTCTGGGTGACGTTATCA 801
QY 257 ----- 257
Db 802 AGTGTAGTGTAGGCCCATGAGATGCTTACAGATCCTAGAACTATGATGAAATTG 861
QY 258 -----HisValAsnGlyGlnProTyrProPheLeuAsnValAl 270
Db 862 TGCATGCTCTAACCAAGCTGCTATACAG--AACGCTAGCGCTTGGCTTATGCTCAAGTGA 920
QY 270 nProArgLysTyrArgPheArgPheLeuAsnAlaAlaValSerArgAlaTyrPheLeuTyr 290
Db 921 GCCGCGCAAGTACCGCTTCCGCTTCTCAGCCGCTCCGCTTCCAGCTTCTTGGCTGTA 980
QY 290 rLeuValAlaArgThrSerSerProAsnValArgIleProPheGlnValIleAlaSerAspAl 310
Db 981 TCTTGCTACCTCTGAGATTCAGAGACCACTTCCCTCCAGTCATGCGCGTACGCG 1040
QY 310 aGlyLeuLeuGlnAlaProValGlnThrSerAsnLeuTyrLeuAlaValAlaGluArgTyr 330
Db 1041 TGGTCTGCTGAGGGCTGTTGACACCTGACACCTGTCATCACTTCTATGCGCGAGCTG 1100
QY 330 rGluIleIleIleAspPheThrAsnPheAlaGlyGlnThrLeuAspLeuArgAsnValAl 350
Db 1101 GGAGGTGTATTCAGCTTCTCCACTTCTGCTGCGCAGTCCAGTCCAGTATCCGAACTTCC 1160
QY 350 aGluThrAsnAspValGlyAspGluAspGluTyrAlaArgThrLeuGlnValMetArgPh 370
Db 1161 TGGTCTGACGCTCGGTGTTGAGCTGAGTTGATTAACCTGACAGATCATGATGCAAT 1220
QY 370 eValValSerSerGlyThrValGlu-----AspAsnSerGlnValProSerThrLeuArg 388
Db 1221 CGTGTGTATGATA--GTCCTTGAAGTGCAGCCGACACTTCTGAGGTGCTGCCAACCTCCG 1277
QY 388 gAspValProPheProHisLysGluGly-----ProAla----- 400
Db 1278 AGATGTTCTTCTCC-----GAGGCGCGCACTGGGAGCCCGCAAAACCCACTGCA 1328
QY 401 -AspLysHisPheLysPheGluArgSerAsnGlyHisTyrLeuIleAsnAspValGlyPh 420
Db 1329 TGACGAGACTTACACTTCGCGCGGTAAATGACAGTGAACATCAACGAGGATTAACCTT 1388
QY 420 eAlaAspValAsnGluArgValLeuAlaLysProGluLeuGlyThrValGluValTyrPgl 440
Db 1389 CTCGGATTCGAGAACCGTCTGCTCCGCAATGTGCCCGCGACACTGTGTGAGATGTGCG 1448
QY 440 uLeuGluAsnSerSerGlyTyrPheHisProValHisIleHisLeuValAspPheLys 460
Db 1449 ACTTGAGAACCACTCAACGCTTGACATCCCTTCTACATTCACCTGCTGATGCTTCG 1508
QY 460 sIleLeuLysArgThrGlyArgGlyValGlnValMetProTyrGluSerAlaGlyLeu 480
Db 1509 AGTCTTCTGCTGCTCACTGCCCGTGA--GTCAGACCTTATGAGGCTGCTGCTCA 1565
QY 480 sAspValValTyrPheLysArgGlyGluThrLeuThrIleGluAlaHisTyrGlnProTyr 500

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Db 1566 GGATGCTGTCTGGCTGCGTCTGCTGAGATGTGTATGTGAGGCCACTACGCTCTTT 1625
QY 500 p-----Thrl 502
Db 1626 -CCCGTAAGTCTCGCCCTTTTAACTTAAGTCTTCTACTCATGCTTAACATCTACAGTGG 1684
QY 502 yAlaTyrMetTyrHisCysHisAsnLeuIleHisGluAspAsnAspMetMetAlaValAlph 522
Db 1685 TGTTCACATAGTTGACATCGCACAACTCATTCACAGAGACCGACATGATGCTGCTTT 1744
QY 522 eAsnValThrAlaMetGluGluLysGlyTyrLeuGlnGluAspPheGluAspPrometAs 542
Db 1745 CAATGTCACTGTCTCGGTGACTGATGCTACAACTACACCGAGTTCATGACCCATGGA 1804
QY 542 nProLysTyrArgAlaValProTyrAsnArgAsnAspPheHisAlaArgAlaGlyAsnPh 562
Db 1805 GCCTCTCTGAGAGCCCGCCCTTCTCTCTGCGAGAGTTCGAGATGGCTCGGGTACTT 1864
QY 562 eSerAlaGluSerIleThrAlaArgValGlnGluLeuAlaGluGlnGluProTyrAsnArg 582
Db 1865 CAGCAGCTTGCCATCACTGACCGCATTCAGAGATGGCTAGCTTCAACCCCTACGCCCA 1924
QY 582 gLeuAspGlu 585
Db 1925 GCGTGTATGAT 1934

RESULT 9
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; Sequence 3, Application US/09401476
; Patent No. 6168936
; GENERAL INFORMATION:
; APPLICANT: Wang, Huang
; TITLE OF INVENTION: No. 6168936el Phenol Oxidizing Enzymes
; FILE REFERENCE: GC584
; CURRENT APPLICATION NUMBER: US/09-401,476
; CURRENT FILING DATE: 1999-09-22
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 3
; LENGTH: 2095
; TYPE: DNA
; ORGANISM: Stachybotrys chararum
US-09-401-476-3

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Score: 1620.50 Matches: 331
Percent Similarity: 65.89% Conservative: 67
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Query Match: 50.82% Indels: 83
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QY 77 Lys-----Met-IleI 80
Db 266 AAGTAGTAGTACATTCTATAGCTTACAGAGACCAAGCTGCTAATCACTTCACTACCTG 325
QY 80 eThrAsnProValThrGlyLysAspIleTyrTyrGluIleGluIleLysProPheGlu 100
Db 326 CCCCACCCCAACACTGAGAGAGACATTTGTACTACAGATGAGATGATTAAGCCCTTCTC 385
QY 100 nGlnArgIleTyrProThrLeuArgProAlaThrLeuValGlyTyrAspGlyMetSerPr 120
Db 386 CCACAGATCTACCTGATCTGAGACCGCGCAACATGCTGTGATGATGATGATGATGATGCC 445
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QY 158 pGlyTPAlaGluAspValThrPheProGlyGluTyrLeuAspTyrThrPheProAsn 178
Db 566 TGGTTGGCTGAGGAGACATACCAAGCTGCGAGTACAGAGATTAATCAACCCAGAG 625
QY 178 rGlnSerAlaArgLeuLeuTyrThrHisAspHisAlaPheMetIleThrAlaGluAsn 198
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QY 198 aTyrPheGlyGlnAlaGlyAlaTyrIleLeuAsnAspGluAlaGluAspAlaLeuGly 218
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QY 218 uProSerGlyTyrGlyGluPheAspIleProLeuIleLeuThrAlaIleTyrTyrAsn 238
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QY 238 aAspGlyThrLeuArgSerThrGluGlyGluAspGlnAspLeuTyrGlyAspValIle 257
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QY 257 ----- 257
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QY 258 -----HisValAsnGlyGlnProTyrProPheLeuAsnValGlu 270
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QY 270 nProArgLysTyrArgPheArgPheLeuAsnAlaAlaValSerArgAlaThrLeuLeuTyr 290
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QY 310 aGlyLeuLeuGlnAlaProValGlnThrSerAsnLeuTyrLeuAlaValAlaGluArg 330
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QY 330 rGluIleIleIleAspPheThrAsnPheAlaGlyGlnThrLeuAspLeuArgAsnVal 350
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QY 350 aGluThrAsnAspValGlyAspGluAspGluTyrAlaArgThrLeuGluValMetArg 370
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Db 1342 AGATGTTCCTTCCCTCC-----GAGGCGCGCAACTGCGAGACCCGCAAAACCCCACTGA 1392
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Db 1809 CATGTGACCTGCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1868
QY 542 nProLysTyrAlaValAlaProTyrAsnArgAsnAspPheHisAlaArgAlaGlyAsn 562
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QY 582 gLeuAspGlu 585
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RESULT 10
US-09-468-578-8
; Sequence 8, Application US/09468578
; Patent No. 6399329
; GENERAL INFORMATION:
; APPLICANT: Wang, Huaming
; APPLICANT: Bodie, Elizabeth A.
; TITLE OF INVENTION: Phenol oxidizing Enzymes
; FILE REFERENCE: GC561-3
; CURRENT APPLICATION NUMBER: US/09/468, 578
; PRIOR FILING DATE: 1999-12-21
; PRIOR APPLICATION NUMBER: US 09/220, 871
; PRIOR FILING DATE: 1998-12-23
; PRIOR APPLICATION NUMBER: US 09/338, 723
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 8
; LENGTH: 858
; TYPE: DNA
; ORGANISM: Amersporium atrum
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(858)
; OTHER INFORMATION: n = A,T,C or G
US-09-468-578-8

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Score: 666.50 Matches: 150
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Db 62 GATGATGTGGTCTGCTTCT- - - - -GGCAAGTATGATGTACTCTTGCACTGTCTCC 115
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Db 116 AAGCGTACACAGCGGACGCTGACCTCTTCGACCCAGAGAGAGACCGATTCACTGTTC 175
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Job time : 137 secs

GenCore version 5.1.6
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Run on: July 4, 2003, 00:18:42 ; Search time 274 Seconds
(without alignments)
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Ygapop 10.0, Ygapext 0.5
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Delop 6.0, Delext 7.0

Searched: 1085931 segs, 780495707 residues
Total number of hits satisfying chosen parameters: 2171862

Minimum DB seq length: 0
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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	3189	100.0	1791	US-09-338-723A-5	Sequence 5, Appl1
2	3189	100.0	1791	US-10-080-210-5	Sequence 5, Appl1
3	3189	100.0	1791	US-10-080-233-1	Sequence 1, Appl1
4	3056	95.8	2067	US-10-080-233-5	Sequence 5, Appl1

5	3056	95.8	3677	10	US-09-338-723A-1	Sequence 1, Appl1
6	3056	95.8	3677	12	US-10-080-210-1	Sequence 1, Appl1
7	3056	95.8	3677	12	US-10-080-233-3	Sequence 3, Appl1
8	1870	58.6	2063	12	US-10-080-210-6	Sequence 6, Appl1
9	1868	58.6	2905	10	US-09-338-723A-3	Sequence 3, Appl1
10	1868	58.6	2905	12	US-10-080-210-3	Sequence 3, Appl1
11	1620.5	50.8	1958	9	US-09-942-185-1	Sequence 1, Appl1
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13	694.5	21.8	1470	10	US-09-874-200-2204	Sequence 2204, Ap
14	666.5	20.9	858	12	US-10-080-210-8	Sequence 8, Appl1
15	500	15.7	1533	9	US-09-738-626-1053	Sequence 1053, Ap
16	500	15.7	3309400	9	US-09-738-626-1	Sequence 1, Appl1
17	480	15.1	1707	9	US-09-938-842A-186	Sequence 186, Ap
18	395	12.4	9025608	9	US-10-156-761-1	Sequence 1, Appl1
19	329.5	10.3	1446	9	US-10-156-761-2742	Sequence 2742, Ap
20	329.5	10.3	9025608	9	US-10-156-761-1	Sequence 1, Appl1
21	322.5	10.1	669	9	US-10-156-761-751	Sequence 751, Ap
22	282	8.8	1830121	9	US-10-329-960-1	Sequence 1, Appl1
23	204	6.4	510	10	US-09-974-300-6479	Sequence 6479, Ap
24	188.5	5.9	1563	9	US-10-263-819-1	Sequence 1, Appl1
25	171.5	5.4	1500	9	US-10-164-775-4	Sequence 4, Appl1
26	162	5.1	5355	9	US-09-944-160-11	Sequence 11, Appl1
27	151	4.7	1713	9	US-09-938-842A-1910	Sequence 1910, Ap
28	147	4.6	1479	9	US-09-938-842A-1675	Sequence 1675, Ap
29	147	4.6	1479	9	US-09-738-626-3280	Sequence 3280, Ap
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34	112	3.5	1626	9	US-09-938-842A-1754	Sequence 1754, Ap
35	106	3.3	1844	9	US-10-016-647-3	Sequence 3, Appl1
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37	105	3.3	8797	9	US-09-808-602-74	Sequence 74, Appl1
38	105	3.3	8797	9	US-09-808-602-77	Sequence 77, Appl1
39	105	3.3	8797	9	US-09-800-198-62	Sequence 62, Appl1
40	105	3.3	8797	9	US-09-800-198-65	Sequence 65, Appl1
41	104.5	3.3	6142	9	US-10-014-436-1	Sequence 1, Appl1
42	103.5	3.2	1791	9	US-10-213-990-50	Sequence 50, Appl1
43	102.5	3.2	3279	9	US-09-423-126-11	Sequence 11, Appl1
44	102.5	3.2	3597	9	US-09-975-719-104	Sequence 104, Ap
45	102.5	3.2	42235	9	US-09-975-719-1	Sequence 1, Appl1

ALIGNMENTS

RESULT 1
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Sequence 5, Application US/09338723A
Patent No. US20020019038A1
GENERAL INFORMATION:
APPLICANT: Humming, Wang
TITLE OF INVENTION: Phenol Oxidizing Enzymes
FILE REFERENCE: GCS61-2
CURRENT APPLICATION NUMBER: US/09/338-723A
CURRENT FILING DATE: 1999-06-23
PRIOR APPLICATION NUMBER: 09/220,871
PRIOR FILING DATE: 1998-12-23
NUMBER OF SEQ ID NOS: 11
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 5
LENGTH: 1791
TYPE: DNA
ORGANISM: Stachybotrys chartarum
US-09-338-723A-5

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Score: 3189.00
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
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Matches: 594
Conservative: 0
Mismatch: 0
Indels: 0
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Source
9/15/03
rnpb

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QY 441 LeuGluAsnSerSerGlyGlyTyrrSerHisProValHisIleHisLeuValAspPheLys 460
DB 1327 CTCGAGAACTCCTCTGAGGCTGGAGCCACCCCTCCACATTCACCTTGTGACTTCAAG 1386
QY 461 IleLeuLysArgThrGlyLysArgGlyGlnValMetProTyrrGlnSerAlaGlyLeuLys 480
DB 1387 ATCTCAAGCGACTGGTGTGCTGCGCAGGTCAATGCTTACGATCTGCTGCTTAA 1446
QY 481 AspValValTrpLeuGlyArgGlyGluThrLeuThrIleGluAlaHisTyrrGlnProTrp 500
DB 1447 GATGCTGCTGCTGGGAGGAGGTGAGACCTGACCATCGAGGCCACTACCAACCTGG 1506
QY 501 ThrGlyAlaTyrrMetTrpHisCysHisAsnLeuIleHisGluAspAsnAspMetIleAla 520
DB 1507 ACTGAGCTTCACTGAGTGGACCTGTCACAACTCATTCACGAGGATTAACGATATGATGCT 1566
QY 521 ValPheAsnValThrAlaMetGluGluTyrrGlyTyrrLeuGlnGluAspPheGluAspPro 540
DB 1567 GTATTCAACGTCACCGCATGAGAGAGAAGGATATCTTCAAGAGACTTGGAGACCCC 1626
QY 541 MetAsnProLysTrpArgAlaValProTyrrAsnArgAsnAspPheHisAlaArgAlaGly 560
DB 1627 ATGAACCCCAAGTGGCGGCGCTTCTTCAACACGCAACGACTTCCATGCTCGCGCTGA 1686
QY 561 AsnPheSerAlaGluSerIleThrAlaArgValGlnGluLeuAlaGlnGluProTyrr 580
DB 1687 AACTTCTCCGCGGATCATCTGCTCCGAGTGAAGGAGTGGCGGACGAGACCGCTAC 1746
QY 581 AsnArgLeuAspGluIleLeuGluAspLeuGlyIleGluGlu 594
DB 1747 AACCGCTCGATGAGATCTTGAGAGATCTTGAATCGAGAG 1788

RESULT 2
US-10-080-210-5
Sequence 5, Application US/10080210
Patent No. US2002014243A1
GENERAL INFORMATION:
APPLICANT: Wang, Huaming
APPLICANT: Bodie, Elizabeth A.
TITLE OF INVENTION: Phenol Oxidizing Enzymes
FILE REFERENCE: GC561-3
CURRENT APPLICATION NUMBER: US/10/080,210
CURRENT FILING DATE: 2002-02-19
PRIOR APPLICATION NUMBER: US 09/220,871
PRIOR FILING DATE: 1998-12-23
PRIOR APPLICATION NUMBER: US 09/338,723
PRIOR FILING DATE: 1999-06-23
NUMBER OF SEQ ID NOS: 17
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 5
LENGTH: 1791
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: CDNA
US-10-080-210-5

Alignment Scores:

Pred. No.:	0	Length:	1791
Score:	3189.00	Matches:	594
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	100.00%	Indels:	0
DB:	12	Gaps:	0

US-10-080-233-2 (1-594) x US-10-080-210-5 (1-1791)

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QY 1 MetIeuPhelSerThrgInleuAlaAlaSerGlyleuSerGlyValleuGly 20
DB 7 ATGCTGTCAAGTCATGAGCAAGTGGAGCAAGCTCGGGCTCGTGTGAGTCCCTGAGC 66
QY 21 IleProMetAspThrGlySerHisProIleGluAlaValAspProGluValLysThrGlu 40
DB 67 ATCCCATGGACACCGGACCCACCCCATTTGAGGCTGTGATCCCGAAGTGAAGACTGAG 126
QY 41 ValPheAlaAspSerIleuAlaAlaAlaGlyAspAspAspTrpGlySerProProTyr 60
DB 127 GTCTTGGCTACCTCCTCTGCTGTCAGCGGCGATGACAGCTGGGAGTCACTCCATAC 186
QY 61 AsnLeuLeuTyrArgAsnAlaLeuProIleProValLysGlnProLysMetIleIle 80
DB 187 AACTGCTTTACAGGAATGCCCTGCAATTCACCTGTCAAGCAGCCCAAGATGATCAT 246
QY 81 ThrAsnProValThrGlyLysAspIleTyrTyrGluIleGluIleLysProPheGln 100
DB 247 ACCACCTGTCTCACCGGACAGCATTTGGTACTATGATCGAGATCAAGCCATTTTCA 306
QY 101 GlnArgIleTyrProThrIleuArgProAlaThrLeuValGlyTyrAspGlyMetSerPro 120
DB 307 CAAGAGATTACCCCACTGGCCCTGCGCACTCTCGGCTACGATGGCATGAGCCCT 366
QY 121 GlyProThrPheAsnValProArgGlyThrGluThrValAlaArgPheIleAsnAsnAla 140
DB 367 GGCTCACTTTCATGATGTCACAGAGAACAGACTGTAGTTAGTTCAATCAACATGCC 426
QY 141 ThrValGluAsnSerValHisIleuHisGlySerProSerArgAlaProPheAspGlyTyr 160
DB 427 ACCGTGAGAACCTGGTCCATGTCAGCGGCTCCCATCGGCTCCCTTCGATGGTGG 486
QY 161 AlaGluAspValThrPheProGlyGluTyrLysAspTyrTyrPheProAsnTyrGlnSer 180
DB 487 GCTGAAGATGTACCTTCCCTGCGAGTACAGAGATTACTTTCACCACTACCAATCC 546
QY 181 AlaArgLeuLeuTyrTyrHisAspHisAlaPheMetLysThrAlaGluAsnAlaTyrPhe 200
DB 547 GCCCGCTTCTGTGATACCATGACACAGCTTTCATGAAAGCTGCTGGAATGGCTACTTT 606
QY 201 GlyGlnAlaGlyAlaTyrIleIleAsnAspGluAlaGluAspAlaLeuGlyLeuProSer 220
DB 607 GGTGAGGCTGGCCCTACATATCAACGAGAGCTGAGATGCTCTCGGCTCTCCAGT 666
QY 221 GlyTyrGlyGluPheAspIleProLeuIleLeuThrAlaLysTyrTyrAsnAlaAspGly 240
DB 667 GGTATAGCGCATTCATATCCTCTGATCTGACGGCCAAATGATATTAAGCGGAGGT 726
QY 241 ThrLeuArgSerThrgInleuGlyGluAspGlnAspLeuTrpGlyAspValIleHisValAsn 260
DB 727 ACCCTGCGTTCGACGAGGGGTGAGACAGAGACTGTGGGAGATGTCATTCATTCAC 786
QY 261 GlyGlnProTyrProPheLeuAsnValGlnProArgLysTyrArgPheArgPheLeuAsn 280
DB 787 GGCACACCATGCGCTTCTTACATGTCACACCCCGCAAGATCGTTCCATTCCTCAAC 846
QY 281 AlaAlaValSerArgAlaTrpLeuLeuTyrLeuValArgHisSerSerProAsnValArg 300
DB 847 GCTGCGGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 906
QY 301 IleProPheGlnValIleAlaSerAspAlaGlyLeuLeuGlnAlaProValGlnThrSer 320
```

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DB 907 ATTCCTTCCAAAGTCATTCGCTGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 966
QY 321 AsnLeuTyrIleuAlaValAlaGluArgTyrGluIleIleIleAspPheThrAsnPheAla 340
DB 967 AACCTTACCTTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1026
QY 341 GlyGlnThrLeuAspIleuArgAsnValAlaGluThrAsnAspValGlyAspGluAspGlu 360
DB 1027 GCGCAGACTCTTGACCTGCGCCACAGCTTGTGACACCAACATGCTGCGCGCAGAGATGAG 1086
QY 361 TyrAlaArgThrLeuGluValMetArgPheValValSerSerGlyThrValGluAspAsn 380
DB 1087 TACGCTGCACTCTCGAGAGTGAAGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1146
QY 381 SerGlnValProSerThrLeuArgAspValProPheProProHisLysGluProAla 400
DB 1147 AGCAGGTGCTTCCATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1206
QY 401 AspLysHisPheLysPheGluArgSerAsnGlyHisTyrIleuIleAsnAspValGlyPhe 420
DB 1207 GACAGACACTTCAAGTTTGAACGACGACGACGACGACGACGACGACGACGACGACGACGACG 1266
QY 421 AlaAspValAsnGluArgValLeuAlaLysProGluLeuGlyThrValGluValTrpGlu 440
DB 1267 GCGATGTCAATGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1326
QY 441 LeuGluAsnSerSerGlyGlyTyrPheHisProValHisIleHisLeuValAspPheLys 460
DB 1327 CTCGAGAACCTTCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCT 1386
QY 461 IleuLysArgThrGlyGlyArgGlyGluValMetProTyrGlnSerAlaGlyLeuLys 480
DB 1387 ATCTCAAGCAAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1446
QY 481 AspValAlaTrpLeuGlyArgGlyGluThrLeuThrIleGluAlaHisTyrGlnProTyr 500
DB 1447 GATGTCGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1506
QY 501 ThrGlyAlaTyrMetTrpHisLysHisAsnLeuIleHisGluAspAsnAspMetMetAla 520
DB 1507 ACTGAGACTTACATGTCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1566
QY 521 ValPheAsnValThrAlaMetGluGluLysGlyTyrLeuGlnGluAspPheGluAspPro 540
DB 1567 GTATTCACCTCAAGCCGATGAGAGAGAGAGAGATTTTACAGAGAGCTTCGAGAGACCC 1626
QY 541 MetAsnProLysTrpArgAlaValProTyrAsnArgAsnAspPheHisAlaArgAlaGly 560
DB 1627 ATGAAACCCCAAGTGGCGCGCTTCTTACAAACCGCAACGACTTCATGCTCGCGCTGGA 1686
QY 561 AsnPheSerAlaGluSerIleThrAlaArgValGlnGluLeuAlaGluGlnGluProTyr 580
DB 1687 AACCTTCCCGCGAGTCCATCACTGCGCGAGTGGAGAGTGGCGCGAGAGAGAGAGAGAGAG 1746
QY 581 AsnArgLeuAspGluIleLeuGluAspLeuGlyIleGluGlu 594
DB 1747 AACCGCTCGATGATCTGAGAGATCTTGAGATTCGATGAGAGAG 1788
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RESULT 3
US-10-080-233-1
; Sequence 1, Application US/10080233
; Patient No. US20020151450A1
; GENERAL INFORMATION:
; APPLICANT: Wang, Huang
; TITLE OF INVENTION: No. US20020151450A1 Phenol Oxidizing Enzymes
; FILE REFERENCE: GC567
; CURRENT APPLICATION NUMBER: US/10/080,233
; CURRENT FILING DATE: 2002-02-19
; NUMBER OF SEQ. ID NOS: 5
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 1791
; TYPE: DNA

ORGANISM: Stachybotrys sp.
US-10-080-233-1

Alignment Scores:

Pred. No.:	0	Length:	1791
Score:	3189.00	Matches:	594
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	100.00%	Indels:	0
	12	Gaps:	0

US-10-080-233-2 (1-594) x US-10-080-233-1 (1-1791)

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QY 1 MetLeuPheLysSerTTPGlnLeuAlaAlaAlaSerGlyLeuLeuSerGlyValLeuGly 20
Db 7 ATGCTGTTCAAGTATGACGACACTGGACACCTCCGGCTCTGTCGAGTCTCGCC 66
QY 21 IleProMetAspThrGlySerHisProIleGluAlaValAspProGluValIleThrGlu 40
Db 67 ATCCCGAGTGGACACCGGCGACCCCAATTCAGCTGTGATCCCGAAGTGAAGACTGAG 126
QY 41 ValPheAlaAspSerLeuLeuAlaAlaGlyAspAspTPGlnSerProProThr 60
Db 127 GTCTTCGCTGACCTCTCTCTGCTGACAGCGATGCGACTGGAGTCACTCCATAC 186
QY 61 AsnLeuLeuTyrArgAsnAlaLeuProIleProValLysGlnProLysMetIleIle 80
Db 187 AACTGCTTTACAGAAATGCGCTGCATTCACACTGCACAGCAGCCCAAGATGATCAT 246
QY 81 ThrAsnProValIleThrGlyLysAspIleThrTyrGluIleGluIleLysProPheGln 100
Db 247 ACCAACCTCTGACCGGAGACATTTGTGATGATGATGATGATGATGATGATGATGAT 306
QY 101 GlnArgIleTyrProThrLeuArgProAlaThrLeuValGlyTyrAspGlyMetSerPro 120
Db 307 CAAGAGATTACCCCACTTCCGCTCCCACTCTCTGCTGCTGCTGCTGCTGCTGCTGCT 366
QY 121 GlyProThrPheAsnValProArgGlyThrGluThrValValArgPheIleAsnAsnAla 140
Db 367 GGTCTACTTTCATGTTCCCGAGAGAACAGACTGATGATGATGATGATGATGATGATGAT 426
QY 141 ThrValGlnAsnSerValHisLeuHisGlySerProSerArgAlaProPheAspGlyTyr 160
Db 427 ACCGTGGAGACCTGGTCCATCTGACGCTCCCTCCCTCCCTCCCTCCCTCCCTCCCTCC 486
QY 161 AlaGlnAspValIleThrPheProGlyLysTyrAspTyrTyrPheProAsnTyrGlnSer 180
Db 487 GCTGAAGATGAGACTTCCCTCGGGAGATGACAAAGATTACTTCCCACTTACCAATCC 546
QY 181 AlaArgLeuLeuTyrTyrHisAspHisAlaPheMetLysThrAlaGlnAsnAlaTyrPhe 200
Db 547 GCCCGCTTGTGTGTACACAGACACGCTTTCATGAAAGACTGCTGAAAGAGCTACTTT 606
QY 201 GlyGlnAlaGlyAlaTyrIleIleAsnAspGlnAlaGlnAspAlaLeuGlyLeuProSer 220
Db 607 GGTAGAGCTGGCGCTTCAATTATACAGACAGAGCTGGAGTGGCTCTCGCTTCTTCTAGT 666
QY 221 GlyTyrGlyLysPheAspIleProLeuIleLeuThrAlaLysTyrTyrAsnAlaAspGly 240
Db 667 GCGTATGGCGAGTTCGATATCCCTGTGATCTCTGAAGCGCAAGTACTATTAAGCGCGATGCT 726
QY 241 ThrLeuArgSerThrGluGlyGlnAspGlnAspLeuTyrGlyAspValIleHisValAsn 260
Db 727 ACCCTGGCTTCGACCGAGGTGAGAGACAGCACTGTGGGAGATGTCATCCATGTCAC 786
QY 261 GlyGlnProTyrProPheLeuAsnValGlnProArgLysTyrArgPheArgPheLeuAsn 280
Db 787 GGAGAGCGATGCGCTTCTTAAAGCTCAGCGCCGCAAGTAACTCTTCCGATTCCTCAAC 846
QY 281 AlaAlaValSerArgAlaTyrPheLeuTyrIleValArgThrSerSerProAsnValArg 300
Db 847 GCTGCCGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 906
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QY 301 IleProPheGlnValIleAlaSerAspAlaGlyLeuLeuGlnAlaProValGlnThrSer 320
Db 907 ATCTCTTCAAGTATGCTGCTGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 966
QY 321 AsnLeuTyrLeuAlaValAlaGluArgTyrGluIleIleIleAspPheThrAsnPheAla 340
Db 967 AACCTTACCTTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1026
QY 341 GlyGlnThrLeuAspLeuArgAsnValAlaGluThrAsnAspValGlyAspGlnAspGly 360
Db 1027 GCGGAGCTCTTGAAGCTGCGGACGCTTCTGACAGCAAGTTCGCGGAGAGATGAG 1086
QY 361 TyrAlaArgThrLeuGluValMetArgPheValIleSerSerGlyThrValGluAspAsn 380
Db 1087 TACGCTGACCTTCGAGAGTATGAGCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1146
QY 381 SerGlnValProSerThrLeuArgAspValProPheProIleLysGluGlyProAla 400
Db 1147 AGCCAGTCCCTCCACTCTCCGACGCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 1206
QY 401 AspLysHisPheLysPheGluArgSerAsnGlyHisTyrLeuIleAsnAspValGlyPhe 420
Db 1207 GACAGACCTTCAAGTTTGAACGACGACGACGACGACGACGACGACGACGACGACGACG 1266
QY 421 AlaAspValAsnGluArgValIleuAlaLysProGluLeuGlyThrValGluValTyrGlu 440
Db 1267 GCCATGTCATGAGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1326
QY 441 LeuGlnAsnSerSerGlyLysTyrSerHisProValHisIleHisLeuValAspPheLys 460
Db 1327 CTCGAGAACCTCTCTGAGGCTGAGGACCCCGCTCCATTCACCTTGTGACTTCAAG 1386
QY 461 IleLeuLysArgThrGlyLysArgGlyGlnValMetProTyrGlnSerAlaGlyLeuLys 480
Db 1387 ATCTCAAGCAAGTACGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1446
QY 481 AspValValTyrPheGlyArgGlyLysThrLeuThrIleGluAlaHisTyrGlnProTyr 500
Db 1447 GATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1506
QY 501 ThrGlyAlaTyrMetThrPheHisAsnLeuIleHisGlnAspAsnAsnMetAla 520
Db 1507 ACTGAGCTTACATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1566
QY 521 ValPheAsnValIleThrAlaMetGluGluLysGlyTyrLeuGlnGlnAspPheGluAspPro 540
Db 1567 GTATTCAACGTCACCGCATGAGAGAGAGATATCTTCAAGAGACTTTCGAGACCC 1626
QY 541 MetAsnProLysTyrPheAlaValProTyrAsnArgAsnAspPheHisAlaArgAlaGly 560
Db 1627 ATGAACCCCAAGTGGCGCGCTTCTTACACCGCAACGACTTCCATGCTCGCGCTGGA 1686
QY 561 AsnPheSerAlaGlnSerIleThrAlaArgValGlnGluLeuAlaGlnGluGlnProTyr 580
Db 1687 AACTTCTCCCGGAGTCCATCTACTGCCGAGTGCAGAGAGTGGCGGAGAGAGAGAGAG 1746
QY 581 AsnArgLeuAspGluIleLeuGlnAspLeuGlyIleGluGln 594
Db 1747 AACCGCTCGATGAGATCCTGAGAGATCTTGAAATCGAGAG 1788
```

RESULT 4

US-10-080-233-5

Sequence 5, Application US/10080233

Patent No. US20020151450A1

GENERAL INFORMATION:

APPLICANT: Wang, Huaming

TITLE OF INVENTION: NO. US20020151450A1 Phenol Oxidizing Enzymes

FILE REFERENCE: G0567

CURRENT APPLICATION NUMBER: US/10/080,233

CURRENT FILING DATE: 2002-02-19

NUMBER OF SEQ ID NOS: 5

SOFTWARE: FastSeq for Windows Version 4.0

SEQ ID NO 5

LENGTH: 2067
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: plasmid
US-10-080-233-5

Alignment Scores:

Score:	0	Length:	2067
Percent Similarity:	3056.00	Matches:	593
Best Local Similarity:	86.70%	Conservative:	0
Query Match:	86.70%	Mismatches:	1
	95.83%	Indels:	91
	12	Gaps:	5

US-10-080-233-2 (1-594) x US-10-080-233-5 (1-2067)

1 MetLeuPheLysSerTrpGlnLeuAlaAlaSerGlyLeuLeuSerGlyValLeuGly 20
10 ATGCTGTCAAGCATGGCAACTGGCAGACCTCCGGGCTCCTGCTGGAGTCTCGGC 69
21 IlePrometAspThrGlySerHisProIleGluAlaValAspProGluValIleThrGlu 40
70 ATCCCGATGGACACCGGACACCCCACTTGGAGCTGTGATCCGAAAGTGAAGACTGAG 129
41 ValPheAlaAspSerLeuAlaAlaAlaGlyAspAspAspTrpGluSerProProTyr 60
130 GTCTTGCTGACTCCCTCCTGCTGCTGACAGCGGATGACAGTGGAGTACCTCCATAC 189
61 AsnLeuLeu-----Tyr 64
190 AACTGCTTACAGTGGAGACACCTGCCACCTGTTTCCCTGATTAACCTAT 249
65 ArgAspAlaLeuProIleProProValLysGlnProLysMet----- 78
250 AGGAATGCCCTGGCAATTCACCTGTCAAGCAGCCCAAGATGATGCTTTGATTTCTA 309
79 -----IleIleThrAsnProValThrGly 87
310 CGAAGACACTCGGCCCCGCACTATGATTTCTAGATCATTTACCAACCTGTCCACCGCAA 369
87 sAspIleTrpTrpTyrGluIleGluIleLysProPheGlnGlnArg----- 102
370 GGACATTTGGTACTATGAGATCGAGATCAAGCCATTTCAAGCAAGGATGGATTTGCTCAG 429
103 -----IleTyrProThrIleuArgpr 109
430 AAACCTTGGTAAATTAATCATTGTTACTGACCCCTTTCAGATTTACCCCACTGGGCC 489
109 oAlaThrLeuValGlyTyrAspGlyMetSerProGlyProThrPheAsnValProArg 129
490 TGGCACTCGTGGGCTAGCATGGCATGGACCCCTGGTCTCACTTTCATTTCCCAAGG 549
129 yThrGluThrValValArgPheIleAsnAsnAlaThrValGluAsnSerValHisLeu 149
550 AACAGAGACTGTAGTGGTTCATCAACAATGCCACCGTGGAGAACCTCGGTCCATCTGCA 609
149 sGlySerProSerArgAlaProPheAspGlyTrpAlaGluAspValThrPheProGly 169
610 CGGCTCCCATCGCGCGCCCTTTCATGGTGGCTGGAAGATGATGACCTTCCCTGGCGA 669
169 uTyrIleAspTyrTyrPheProAsnTyrGlnSerAlaArgLeuLeuTrpIleHisAsp 189
670 GTACAGAGATTAATCTTCCCAATACCAATCCGCGCTCTGTGGTACATAGCA 729
189 sAlaPheMetLys----- 193
730 CGCTTTCATGAA-GGATGCTACGAGCCCTTATCTTTCGCTACCTTTGGCTAACCA 788
194 -----ThrAlaGluAsnAlaTyrPheGlyGlnAlaGlyAlaTyrIleIleAs 209
789 CTTCCTTTGCTGAGACTGCTGAGAAATGCTTACTTTGGTCAAGGCTGGCGCTACATTAACA 848

209 nAspGluAlaGlyAspAlaLeuGlyLeuProSerGlyTyrGlyLysPheAspIleProle 229
849 CGACGAGGCTGAGAGATCTCTCGTCTTCTAGAGGCTATGGAGATGATATTCCTCT 908
229 uIleLeuThrAlaLysTyrTyrAsnAlaAspGlyThrLeuArgSerThrGluGluAs 249
909 GATCTGACGCGCCAGACTATTAACCGCATGGTACCTCCCTCGACCAAGGCTGAGGA 968
249 pGluAspLeuTrpGlyAspValIleHisValAsnGlyGlnProTrpProPheLeuAsn 269
969 CAGAGACTGTGGGAGATGTCATCCATGTCAAGGGACAGCCATGGCTTTCTTACAGT 1028
269 lGlnProArgLysTyrArgPheArgPheLeuAsnAlaAlaValSerArgAlaTrpLeu 289
1029 CAGCCCCGCAATACCGTTCCGATTCCTCAACGGCTGGCTGTCTGCTGGCTCT 1088
289 uTyrLeuValArgThrSerSerProAsnValArgIleProPheGlnValIleAsnSer 309
1089 CTACCTGCTGGAGACAGCTCTCCCAACGTCAAGAAATTCCTTCCAAAGTCAATGCCCTGA 1148
309 pAlaGlyLeuLeuGlnAlaProValGlnThrSerAsnLeuTyrLeuAlaValAlaGlu 329
1149 TGCTGGTCTCTTCAAGCCCCCGTTCAGACTCTTAACCTTACCTTGTCTTCCGAGCG 1208
329 gTyrGluIleIleIle----- 334
1209 TTACGAGATCATATTATGCTATGCCCTCCCTCCACGAATGAGTCAAGACTATGACT 1268
335 -----AspPheThrAsnPheAlaGlyGlnThrLeuAspLeuArgAsnValAlaG 351
1269 AACACTGTGAGACTTCAACCAATTCGTGCGCCAGACACTTGCAGCTGGCAACGTCTGCA 1328
351 uThrAsnAspValGlyAspGluAspGlyLysTrpAlaArgThrLeuGluValMetArgPhe 371
1329 GACCAAGATGTGGGAGACAGATGATGAGCTCGACACTGTGAGGTATGGCTTCGT 1388
371 ValSerSerGlyThrValGluAspAsnSerGlnValProSerThrLeuArgAspVal 391
1389 CGTCAGCTGTGGACAGTGTAGGACCAACACACAGGTCCTCCACACTCTCCGTACGTTCC 1448
391 oPheProProHisLysGlyLysProAlaAspLysHisPheLysPheGluArgSerAsn 411
1449 TTTCCTCTCCACAAAGAGGCCCGCCGCAAGCACTTCAAGTTTGCAACGCAACAGG 1508
411 yHisTyrLeuIleAsnAspValGlyPheAlaAspValAsnGluArgValLeuAlaLys 431
1509 AACACTACCTGATTAACGATGTGGCTTGTGCGATGTCAAGACGCTGCTGGCCAAAGCC 1568
431 oGluLeuGlyThrValGluValTrpGluLeuGluAsnSerSerGlyTyrPheSerHis 451
1569 CGAGCTCGGACCGGTTGAGGTCGGAGAGCTCGAAGACTCCTCGAGAGCTGGAGCAACC 1628
451 oValHisIleHisLeuValAspPheLysIleLeuLysArgThrGlyLysArgGlyGln 471
1629 CGTCCACATTCACCTTGTGACTTCAAGATCCCAAGCGAATCGGTGGTGGCCAGGT 1688
471 lMetProTyrGluSerAlaGlyLeuLysAspValValTrpLeuGlyArgGlyGlnThr 491
1689 CATGCCCTAGCAATCTGCTGTCTTAAGATGTGCTGTGGTGGCGAGGGGTAGACCT 1748
491 uThrIleGluAlaHisTyrGlnProTrpThrGlyAlaTyrMetTrpHisCysHisAsn 511
1749 GACCAATGAGGCCCACTACCAACCTGGAGCTGAGGTATGAGTGGAGCTGCACAACCT 1808
511 uIleHisGluAspAsnAspMetLeuAlaValPheAsnValThrAlaMetGluGlyGln 531
1809 CATTCACGAGGATTAACGATGCTGATTAATCAACGTCACCGCATGAGAGAGAGAGG 1868
531 yTyrLeuGlnGluAspPheGluAspProMetAsnProLysTrpArgAlaValProTyr 551
1869 ATATCTTCAGAGAGACTTCCAGAGCCCATGAACCCCAAGTGGCGGCTTCTTACAA 1928
551 nArgAsnAspPheHisAlaArgAlaGlyAsnPheSerAlaGluSerIleThrAlaArg 571

D _b	1929	CCGGAACGACTTCCATCTCGCGGTGGAACTTTCCGCCAGTCATCATCAATTGCCAGT	1988
OY	571	IGInGIuLeuAlaGIuGIuInIuProTYrAsnArgLeuApsCIuILeugInuAsPleuGI	591
D _b	1989	GCAgGAcTGtGCcCAGcAGAgGccGTACCAACGCCCTGATGATCTCGAGGATCTTGG	2048
OY	591	yIIeGIuGIu	594
D _b	2049	AATCGAGGAG	2058

RESULT 5

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US-09-338-723A-1
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: Sequence 1, Application US/09338723A
: Patent No. US20020019038A1
:
: GENERAL INFORMATION:
:
: APPLICANT: Humming, Wang
:
: TITLE OF INVENTION: Phenol Oxidizing Enzymess
:
: FILE REFERENCE: GCG61-2
:
: CURRENT APPLICATION NUMBER: US/09/338,723A
:
: PRIOR FILING DATE: 1999-06-23
:
: PRIOR APPLICATION NUMBER: 09/220,871
:
: PRIOR FILING DATE: 1998-12-23
:
: NUMBER OF SEQ ID NOS: 11
:
: SOFTWARE: FastSeq for Windows Version 3.0
:
: SEQ ID NO 1
:
: LENGTH: 3677
:
: TYPE: DNA
:
: ORGANISM: Stachybotrys chartarum
:
: US-09-338-723A-1

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Alignment Scores:

Pred. No.:	0	Length:	3677
Score:	3056.00	Matches:	593
Percent Similarity:	86.70%	Conservative:	0
Best Local Similarity:	86.70%	Mismatches:	1
Query Match:	95.83%	Indels:	91
DB:	10	Gaps:	5

US-10-080-233-2 (1-594) x US-09-338-723A-1 (1-3677)

QY	1	MetLeuPheYsSerTPgiLnLeuAlaAlaSerGlyLeuSerGlyValLeuGly	20
Db	1044	ATGCTGTTCAGTCAATGAGACACTGGACGACCTCCGGGCTCTGTCTGGAGTCTCGGGC	1103
QY	21	IleProMetAspThrGlySerHisProIleGluAlaValAspProGluValLysThrGlu	40
Db	1104	ATCCCGATGGACACCGGACGACCCACCATTGAGGCTGTGATCCCGAAGTGAACATCGAG	1163
QY	41	ValPheAlaAspSerLeuLeuAlaAlaGlyAspAspAspTrpGluSerProProTyr	60
	1164	GTCCTGGCTGACTCCCTCTCTGTGTGACGACGGCGATGACATCGGGAGTCACTCCATAC	1223
QY	61	AsnLeuLeu-----Tyr	64
Db	1224	AACTTGCTTACAGGTGAGACACCTGTCCACCGTGTTCCTCGATTAACACTCTTAT	1283
QY	65	ArgAsnAlaLeuProIleProProValLysGlnProLysMet-----	78
Db	1284	AGGAATGACCTCGCAATTCACCTGTCACGACCCCAAGATGATGCTTGGATTTCTA	1343
QY	79	-----IleIleThrAsnProValThrGly	87
Db	1344	CGAAGCACTCGGGCCCGACTAATGTATTCTTAGGATCATTAACCAACCTGTCAACGGGCAA	1403
QY	87	SAspIleTrpTyrTyrGluIleGluIleLysProPheGlnGlnArg-----	102
Db	1404	GGACATTTGGTACTATGATGATGAGATCAAGATCAAGCATTTACAGCAAAAGGGTGATTTGCTAC	1463
QY	103	-----IleTyrProThrIleuArgPr	109
Db	1464	AAACCTTGGTGAATTATATCATTTGTACTGACCCCTTTCAGATATTTACCCCACTTTCGCCCC	1523

QY	109	oLaAThrlEuaValGlyTyrAspGlyMetSerProGlyProThrPheAsnValProArgI	129
Db	1524	TGCACACTCTGTGGCGCATGACATGGACCCCTGGCTCTACTTTCATCTTCCAGAGG	1583
QY	129	yThrGluThrValValAlaRppHeiLeaAsnAlaThrValGluAsnSerValHsLeuH	149
Db	1584	AACGAGACAGTGAATGTGGTTCAATCAACAMGCAACCGTGGAGAACTCGGTCAATCGCA	1643
QY	149	sGlySerProSerArgIaIaProPheAspGlyTTPAlaGluAsnValThrPheProGlyI	169
Db	1644	CGGGTCCCAATCGGTGCCCTTCGATGGGTGGGCTGAAGAATGTGACTTCCCTGGCGCA	1703
QY	169	uTYrLYAspTYrTYrPheProAsnTYrGlnSerAlaArgLeuLeuTYrPyrHsAspH	189
Db	1704	GTACAAAGATTAAGTACTTTCACCAATCCAGCAATCGCGGCTCTGGTGAACATGACCA	1763
QY	189	sAlaPheMetLys-----	193
Db	1764	CGCTTTTCATGAA-GGTAAWGCTACGAGCCCTTAATCTTCTGGCTACTTGGCTAAACAA	1822
QY	194	-----ThrAlaGluAsnAlaTYrPheGlyGlnAlaGlyAlaTYrIleLea	209
Db	1823	CTTCCTTTCGTAGACTCTGAGAAATGGCTACTTGGTCAGAGCGGGCGCTCAATATACAA	1882
QY	209	nAspGluAlaGluAspAlaLeuGlyLeuProSerGlyTYrGlyGluPheAspIleProIe	229
Db	1883	CGAGGAGCGAGAGATGCTCTCGGTCTCTCTACTAGGCTAAGGAGAGTTCATATCCCTCT	1942
QY	229	uIleLeuThrAlaLysTYrTYrAsnAlaAspGlyTYrThrLeuAsrSerThrGluGlyLys	249
Db	1943	GATCTACAGCGCCACAGTACTATTAACGCCGATGGTACCCTCGCTTCACGCGAGGTAGCA	2002
QY	249	pGlnAspLeuTYrPdpLYAspValIleHsValaGlnGlyGlnProTYrProPheLeuAsnVa	269
Db	2003	CCAGGAGACCTGTGGGAGATGTCAATCCATGTCAACGAGCAGCAGCAGTGGGCTTCTTAAGT	2062
QY	269	IgInProArgLysTYrArgPheArgPheLeuAsnAlaAlaValSerArgAlaIrrPheLeu	289
Db	2063	CCAGCCCCCGAAGTACCGTTCGATTCGATTCGCAACGCGTGGCTGTCTGTGGCTCTCT	2122
QY	289	uTYrLeuValArgThrSerSerProAsnValArgIleProPheGlnValIleAlaSerAs	309
Db	2123	CTACCTGCTGAGGACCAAGCTCTCCCAACGTCAGAAATTCCTTCCAAAGTATGCTCTGTA	2182
QY	309	pAlaGlyLeuLeuGlnAlaProValGlnThrSerAsnLeuTYrLeuAlaValAlaGluAr	329
Db	2183	TGCTGGCTCTCTTCAACGCCCGCTTCAGACTTCAACTCTTACCTTGCTGTGTCGAGCG	2242
QY	329	gTYrGluIleIleIleIle-----	334
Db	2243	TTTACGAAATCATATTATTTGGTATGGCCCTCCCTCCACGAAATGATCAAGAACTATAGACT	2302
QY	335	-----AspPheThrAsnPheAlaGlyGlnThrLeuAspLeuArgAsnValAlaG	351
Db	2303	AACACTGTATGACTTTCACCAACTTGTGTCGACAGCTCTTGACTCGGCAACCTTCTCTGA	2362
QY	351	uThrAsnAspValGlyAspGluAspGlyuTYrAlaArgThrLeuGluValMetArgPheYa	371
Db	2363	GACCAACGATGTGGCGCAGAGAGATGATAGCTCTGCACTCTCGAGGTGATGTGGCTTCG	2422
QY	371	IValSerSerGlyTYrThrValGluAspAsnSerGlnValProSerThrLeuArgAspValPr	391
Db	2423	CGTCAAGCTCTGGCAGCTTTGAGGACAAACAGCCAGGTGCCCTCCACATCTCGGTGACGTTCC	2482
QY	391	oPheProProHsLysGluGlyProAlaAspLysHsIlePheLysPheGluArgSerAsnG	411
Db	2483	TTTTCCCTCCACAAAGAGGCCCGCCGCAAGACACTTCAAGTTTGAACGCGCAACCG	2542
QY	411	yHsIstYrLeuIleAsnAspValGlyPheAlaAspValaGlnArgValLeuAlaLysPr	431
Db	2543	ACACTACTCTATCAAGATGTTGGCTTTGGCAATGTCAATGACGCTGTCTGGCCAAAGCC	2602
QY	431	oGluLeuGlyThrValGluValAlaIrrPdpIleuGluAsnSerSerGlyGlyTYrSerHsIpr	451

Db	1104	ATCCGATGGACACCGGAGCGCACCCCATTTAGAGCTGTGTGATCCCGAAGTGAACACTGAG	1163
QY	41	ValPheAlaAspSerLeuLeuAlaAlaGlyaspaspaSPTrpGluSerProProTrp	60
Db	1164	GTCCTCCCTGACTCCCTCCCTTGCTGACAGCAGCGCATGACGACTGAGTCCACTCCATAC	1223
QY	61	AsnLeuLeu-----Tyr	64
Db	1224	AACTTGGCTTACAGGTGAGACACTGTCCCACTGTTTCCCTGGATTAACATACTTAT	1283
QY	65	ArgAsnAlaLeuProIleProProValLysGlnProLysMet-----	78
Db	1284	AGGAATGCCCTGGCAATTCGACCTGTCAAGCAGCCCAAGATGTATGTCTTGATTTCTTA	1343
QY	79	-----IleLeuThrAsnProValIleTrpGly	87
Db	1344	CGAAGCACTCGGCGCCGCACTAATGTATTTGATGATCAATTAACAACCTGTGCACCGGCA	1403
QY	87	saSPileTrpTyrGluIleGluIleLysProPheGlnIleArg-----	102
Db	1404	GGACATTTTGGTACTATGAGATCGAGATCAACACCTTTCAGCAAAAGGAGATTGGCTCAG	1465
QY	103	-----IleTyrProThrLeuAlaPr	109
Db	1464	AAACCTTGTTGGTAATTAATCATTTGTACTACGACCTTTCAGATTTTATACCCCACTTGGCCGC	1523
QY	109	oAlaThrLeuValIleTyrAspGlyMetSerProGlyProThrPheAsnValProArgGly	129
Db	1524	TGCCACTCTGTCGGCTACGATGGCATGAGCCCTGGTCTCTACTTTCAATGTTCCCAAGG	1583
QY	129	YThrGluThrValValArgPheIleAsnAsnAlaThrValGluAsnSerValIleAsnIle	149
Db	1584	AACAGACACTGTACTGTAGTTCATCAACAAGCAGCCGTGAGAACTGGGTCAATCTCA	1643
QY	149	sglySerProSerArgAlaProPheAspGlyTTrpAlaGluAspValThrPheProGlyIle	169
Db	1644	CGGCTCCCACTGGGTGCTCCCTTTCGATGGTGGGGCTGMAATGTGACCTTCCCTGGCGCA	1703
QY	169	uTYLysAspTyrTyrPheProAsnTyrGlnSerAlaArgLeuLeuTrpTyrIleAspH1	189
Db	1704	GTACAAGATTACTACTTTCACACTACATCCGCCGCTTGTGTGATCAATGACCA	1763
QY	189	sAlaPheMetLys-----	193
Db	1764	CGCTTTCATGAA--GGTATGCTACGAGCCTTATCTTCTTGGCTACCTTGGCTAACCA	1822
QY	194	-----ThrIleGluAsnAlaTyrPheGlyGlnAlaGlyIleAlaTyrIleIleAs	209
Db	1823	CTTCCCTTTCGTAGACTGCTGAGAAATGCCCTTATGGTCAAGCTGCGCTACATTAATCAA	1882
QY	209	naSPGluAlaGluAspAlaLeuGlyLeuProSerGlyTyrGlyIleupheAspIleProLe	229
Db	1883	CGAAGAGAGCTGAGGATGCTCTCGGCTTCTCCATGAGGCATATGGCAATTCGATATCCCTCT	1942
QY	229	uIleLeuThrAlaLysTyrTyrAsnAlaAspGlyThrLeuArgSerThrGluGlyIleAs	249
Db	1943	GATCTCAAGCGCCAGTACTATAACGCCGAGATGTAACCTGGCTTGCAGCCGAGGTGAGGA	2002
QY	249	pgIAspLeuTrpGlyAspValIleAsnValAsnGlyGlnProTrpProPheLeuAsnVal	269
Db	2003	CAAGGACTGTGGGGAATGTCAATCCATATGCAAGCAAGCAAGCAAGCAAGCGCTTCCATTAAGT	2062
QY	269	IcGlnProArgLysTyrArgPheArgPheLeuAsnAlaAlaValSerArgAlaTrpLeuLe	289
Db	2063	CCAGCCCCCGAAGTACCGTTCATTCCTTCACAGCGCGCTGTCTGTGGCTTGGCTCT	2122
QY	289	uTYrLeuValAlaArgThrSerSerProAsnValArgIleProPheGlnValIleAlaSerAs	309
Db	2123	CTACCTGTGAGAGCAAGCTCTCCCAACGTCAAGAAATTCCTTTCCAAGTCAATGGCTCTGA	2182
QY	309	paIaGlyLeuLeuGlnAlaProValGlnThrSerAsnLeuTyrLeuAlaValAlaGluArg	329

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Db      2183 TCGTGGTCTCTTCACGCCCGGTCAGACCTTAACCTTACCTTGTGTCGAGCG 2242
Qy      329 GTTGTGTTTlellele----- 334
Db      2243 TTACAGATCATATTATTGGTATGCCCTCCCTCTCAGATGATGATGAAGACTCTAAGACT 2302
Qy      335 -----AspPheThrAsnPhenAlaGlyGlnThrLeuAspLeuArgAsnValAlaGly 351
Db      2303 AACACTGTGACTCTCACCAACTTGTGCGCAGACTCTTGACCTGCGCAACGTTGCTGA 2362
Qy      351 uThrAsnAspValGlyAspGlyAspGlyTyrAlaArgThrLeuGlyValMetArgPheVa 371
Db      2363 GACCAACGATGTGCGGAGAGAGATGATGACCTGCACTCTGAGGTGATCGCTGCT 2422
Qy      371 ValSerSerGlyThrValGlyAspAsnSerGlnValProSerThrLeuArgAspValPr 391
Db      2423 CGTCAGCTCTGGCACTGTGAGAGACACAGCCAGGTCCCTCTCACTCTCCGTGACGTTCC 2482
Qy      391 OPheProRoHisLysGlyGlyProAlaAspLysHisPheLysPheGlyArgSerAsnGly 411
Db      2483 TTTCCCTCCTCACAAGAAAGGCCCGCGCAGACACTTCAAGTTTGAACGACGACGAG 2542
Qy      411 YHisThrLeuLeuAsnAspValGlyPheAlaAspValAsnGlyValGlyValAlaLysPr 431
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Qy      431 OGluLeuGlyThrValGlyValThrPgluLeuGlyAsnSerSerGlyGlyTyrSerHisPr 451
Db      2603 CGAGCTCGGACCGCTTGAAGTCTGGAGCTCGAGAACCTCTGTGAGGCTGAGGCCACCC 2662
Qy      451 OValHisThrLeuValAspPheLysIleLeuLysArgThrGlyGlyArgGlyGlyVal 471
Db      2663 CGTCACACTTCACCTTGTGACTTCAAGATCTCAAGGAACTGTGGTGGCGGACAGT 2722
Qy      471 LMeProTyrGlyGlySerAlaGlyLeuLysAspValValThrLeuGlyArgGlyGlyThrLe 491
Db      2723 CATGCCCTACGAGTGTGCTGAGATGCTGTGAGGCTGTGGTGGGAGGAGGAGACCT 2782
Qy      491 uThrIleGlyAlaHisThrGlyGlnProTyrThrGlyAlaTyrMetThrPheHisAsnLe 511
Db      2783 GACCATTCAGAGGCCCTACCAACCTTGAGCTGAGACTTACATGTCGACTGTGACAACT 2842
Qy      511 uIleHisGlyAspAsnAspMetMetAlaValPheAsnValThrAlaMetGlyGlyGlySGI 531
Db      2843 CATTCACAGAGATTAACAGATGATGCTGTATTCACCTCACCGCATGAGAGAGAGAGG 2902
Qy      531 YTyrIleuGlnGlyAspPheGlyAspProMetAsnProLysTyrPheAlaValProTyrAs 551
Db      2903 ATATCTTCAGAGGACTTCGAGAGACCCCATGAAACCCCAAGTGCGCGCTTCTTACAA 2962
Qy      551 nArgAsnAspPheHisAlaArgAlaGlyAsnPheSerAlaGlySerIleThrAlaArgVa 571
Db      2963 CCGCAACGACTTCCTGCTGGCGGAGAACTTTCGCCGCGATCCATCACATCGCCGAGT 3022
Qy      571 IGlnGlyLeuAlaGlyGlnGlyProTyrAsnArgLeuAspGlyIleLeuGlyAspLeuGI 591
Db      3023 GCAGAGCTGCGCGAGCAGAGACCTTACAAACCGCTCATGATGATCTGAGAGATCTTGG 3082
Qy      591 YIleGlyGly 594
Db      3083 AATCGAGGAG 3092

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; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 3677
; TYPE: DNA
; ORGANISM: Stachybotrys chartarum
; US-10-080-233-3

Alignment Scores:
Score: 0
Pred. No.: 3056.00
Percent Similarity: 86.70%
Best Local Similarity: 86.70%
Query Match: 95.83%
DB: 12 Gaps: 5

US-10-080-233-2 (1-594) x US-10-080-233-3 (1-3677)

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Qy      21 IleProMetAspPheGlySerHisProIleGlyAlaValAspProGlyValLysThrGly 40
Db      1104 ATCCGATGAGACACCGGAGCCACCCCATTTGAGGCTTTGATCCGAAAGTGAAGACTGAG 1163
Qy      41 ValPheAlaAspSerLeuLeuAlaAlaGlyAspAspTrpGlySerProTyr 60
Db      1164 GCTTCGCTGACTCCCTCTTCTGCTGACAGCGCATGACGACTGGAGATCACTCATATC 1223
Qy      61 AsnLeuLeu-----Tyr 64
Db      1224 AACTTGTTCACAGGTGAGACACACTGTCCACCTGTTCCTCGATTAACATACTTAT 1283
Qy      65 ArgAsnAlaLeuProIleProProValLysGlnProLysMet----- 78
Db      1284 AGGAATGCCCTGCGCAATTCACCTGTCAAGCAGCCCAAGATGATGCTTTGATTCTTA 1343
Qy      79 -----IleIleThrAsnProValThrGlyGly 87
Db      1344 CGAAGCAGCTGGCCCGCAGTAAATGATTTCTAGATCAATTACCAACCTGTGACAGCGGAA 1403
Qy      87 SASPIleTrpTyrTyrGlyIleGlyIleLysProPheGlnArg----- 102
Db      1404 GGACATTTGGTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1463
Qy      103 -----IleTyrProThrLeuArgPr 109
Db      1464 AAACCTTGTGATTAATCATTTGTTACTGACCTTTTACGATTTACCCACCTTGGCCCC 1523
Qy      109 OAlaThrLeuValGlyTyrAspGlyMetSerProGlyProThrPheAsnValProArgGly 129
Db      1524 TGCCACTCTCGCGGCTGACATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1583
Qy      129 YThrGlyThrValValArgPheIleAsnAsnAlaThrValGlyAsnSerValHisLeuH 149
Db      1584 AACAGAGACTGTAGTTAGTTATCAACAAAGCCACCTGAGAACTGGGTCATCTGCA 1643
Qy      149 sGlySerProSerArgAlaProPheAspGlyTyrPheAlaGlyAspValThrPheProGlyGI 169
Db      1644 CGGCTCCCATGCGCTGCTGCTTTCGATGATGATGATGATGATGATGATGATGATGATGATGAT 1703
Qy      169 uTyrLysAspTyrTyrPheProAsnTyrGlnSerAlaArgLeuLeuTyrTyrHisAspHI 189
Db      1704 GTACAGAGATTACTACTTCCCACTACCAATCCGCCGCTTCTGTGTGATCAATGACCA 1763
Qy      189 SALAPheMetLys----- 193
Db      1764 CGCTTTCATGAA-GGTATGCTACGAGCCTTATCTTCTTGTGCTACCTTGTGCTAACCA 1822
Qy      194 -----ThrAlaGlyAsnAlaTyrPheGlyGlnAlaGlyAlaTyrIleLeuAs 209
Db      1823 CTTCCTTTCGTAGACTGCTGAGAAATGCTTACTTGTGTGAGCTGGCGCTACATTAACA 1882

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QY 209 nAspGluAlaGluAspAlaLeuGlyLeuProSerGlyTyrGlyGluPheAspIleProle 229
DB 1883 CGACGAGGCTGAGATGCTCGGCTCTCTGATGGGAGATTCGATATCCCTCT 1942
QY 229 uilleuThralAlaLysTyrTyrAsnAlaAspGlyThrLeuArgSerThrGluGlyLys 249
DB 1943 GATTCCTGAGGCGCAAGTACTATACGCCATGCTACCGCTTCACCGAGGCTGAGA 2002
QY 249 pGlnAspLeuTyrGlyAspValIleHisValAsnGlyGlnProTyrProPheLeuAsn 269
DB 2003 CGAGGAGCTGTGGGAGATGATCATCTCATCGAGAGAGCCATGGCTTCTCTTACG 2062
QY 269 lGlnProArgLysTyrArgPheArgPheLeuAsnAlaAlaValSerArgAlaTyrPhe 289
DB 2063 CGAGGCGCGCAGATGACCTTCGATCTCTCAACGCTGCGGCTCGTGGCTGCTCT 2122
QY 289 uTyrLeuValArgThrSerSerProAsnValArgIleProPheGlnValIleAlaSer 309
DB 2123 CTACCTCGCAGAGACAGCTCTCCCAACCTCAGAAATTCCTTCCAAAGTATGCTCTGA 2182
QY 309 pAlaGlyLeuLeuGlnAlaProValGlnThrSerAsnLeuTyrLeuAlaValAlaGlu 329
DB 2183 TCTGTGCTCTTCAAGCCCCGCTTCAGACTCTTACCTTACCTTGTGTGCGAGCG 2242
QY 329 gTyrGluIleIleIleIleIleIleIleIleIleIleIleIleIleIleIleIleIle 334
DB 2243 TTACGAGATCATTTATGCTATGCTCCCTCCCTCAGATGATGATCAAGACTCTAGACT 2302
QY 335 -----AspPheThrAsnPheAlaGlyGlnThrLeuAspLeuArgAsnValAlaG 351
DB 2303 AACACTTGATGACTTCACCAACCTTCTGCTGCGAGACTCTTGAACCTGCGCAGCTGCTGA 2362
QY 351 uThrAsnAspValIleGlyAspGluAspGluTyrAlaArgThrLeuGluValMetArgPhe 371
DB 2363 GACCAACAGATGCTCGGCGAGAGAGATGATGCTGCTGCTGCTGAGATGATGCTGCTGCT 2422
QY 371 lValSerSerGlyThrValGluAspAsnSerGlnValProSerThrLeuArgAspVal 391
DB 2423 CCGTCAAGCTCTGCGACGTTGAGAGACAAAGCGGCTCCCTCAGCTCTCGGAGCTTGC 2482
QY 391 oPheProProHisLysGlyGlyProAlaAspLysHisPheLysPheGluArgSerAsn 411
DB 2483 TTTCCCTCTCACAAGGAGGCGCGCGCAGCAAGCACTTCAAGTTTGAACGAGCAGCAACG 2542
QY 411 yHisTyrLeuIleAsnAspValIleGlyPheAlaAspValAsnGluArgValLeuAlaLys 431
DB 2543 ACACTAACCTGATCAACGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2602
Y 431 oGluLeuGlyThrValGluValTyrPGLuLeuGluAsnSerSerGlyLysTyrSerHis 451
DB 2603 CGAGCTCGGCGACGTTGAGGCTGTGGAGCTCGAGAACTCTCTGAGAGCTGTGGAGCCACCC 2662
QY 451 oValHisIleHisLeuValAspPheLysIleLeuLysArgThrGlyLysValGlyLys 471
DB 2663 CCGTCAACATTCACCTGTTGACTTCAAGATCTCAAGCAACACTGTGGGCTGTGGCGACGT 2722
QY 471 lMetProTyrGluSerAlaGlyLeuLysAspValValTyrPGLuArgGlyLysVal 491
DB 2723 CATGCCCTACGAGCTGCTGCTGCTTACGATGCTGCTGCTGCTGCTGCTGCTGCTGCT 2782
QY 491 uThrIleGluAlaHisTyrGlnProTyrThrGlyAlaTyrMetTyrHisCysHisAsn 511
DB 2783 GACCAATCGAGGCGCCACTACCAACCCGAGCTGTGAGCTGTGAGCTGTGAGCTGTGAGCT 2842
QY 511 uIleHisGluAspAsnAspMetMetAlaValPheAsnValThrAlaMetGluGluLys 531
DB 2843 CATTCACGAGGATACGACATGATGCTGTATTCACAGCTCACCGCATGAGAGAGAGG 2902
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DB 2903 ATATGCTTCAGAGAGACTTGGAGAGCCCAATGAAACCCCAAGTGGCGGCTGCTTACCA 2962
QY 551 nArgAsnAspPheHisAlaArgAlaGlyAsnPheSerAlaGluSerIleThrAlaArg 571

DB 2963 CGCAACGACTTCATGCTCGCGCTGAAACCTTCGCGCGATCATCATGCGGAGT 3022
QY 571 lGlnGluLeuAlaGluGlnGluProTyrAsnArgLeuAspGluIleLeuGluAsp 591
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QY 591 yIleGluGlu 594
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RESULT 8
US-10-080-210-6
; Sequence 6, Application US/10080210
; Patent No. US20020142423A1
; GENERAL INFORMATION:
; APPLICANT: Wang, Huming
; APPLICANT: Bodle, Elizabeth A.
; TITLE OF INVENTION: Phenol Oxidizing Enzymes
; FILE REFERENCE: GC561-3
; CURRENT APPLICATION NUMBER: US/10/080,210
; PRIOR FILING DATE: 2002-02-19
; PRIOR APPLICATION NUMBER: US 09/220,871
; PRIOR FILING DATE: 1998-12-23
; PRIOR APPLICATION NUMBER: US 09/338,723
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 6
; LENGTH: 2063
; TYPE: DNA
; ORGANISM: Curvularia pallescens
US-10-080-210-6
Alignment Scores:
Pred. No.: 3,1e-211 Length: 2063
Score: 1870.00 Matches: 365
Percent Similarity: 67.62% Conservative: 82
Best Local Similarity: 55.22% Mismatches: 133
Query Match: 58,648 Indels: 82
DB: 12 Gaps: 11
US-10-080-233-2 (1-594) x US-10-080-210-6 (1-2063)
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DB 67 GCTTTC-----AGCGAGGCTCTGCGCAATATATATGAGAAACCCCGCAGAAAG 120
QY 42 PheAlaAspSerLeuLeuAlaAlaGlyAspAsp----- 53
DB 121 GCTGCC-----CTGCGACACCATCTGGAAGATGACCTGCCGATGTTTCAAGATCTG 174
QY 54 -----AspTyrGluSerProProTyrAsnLeuLeuTyrArgAsnAlaLeuProIlePro 72
DB 175 AAGGATGCGAAAGCCCGGAGATGATCCATCTTTTTCGAGGAGCTGCGCATCCCTGCA 234
QY 73 ValLysGlnProLys----- 77
DB 235 GCCAAGAACCGAAGAGTGAAGCTTGAATGATGATGACAGCTTTCAGATATGCTCA 294
QY 78 -----MetIleThrAsnProValIleThrGlyLysAspIleTyrTyrGluIle 94
DB 295 CCATCCGAGTAAATGAGCAATCTGTACACAAACAGAGATCTGTACTACGAGATT 354
QY 95 GluIleLysProPheGlnGlnArgIleTyrProThrLeuArgProAlaThrLeuValGly 114
DB 355 GTATCAAAACCTTTTAAACAGAGGCTTATCCAAAGTACGTCGCTGCTGCTGATGAGC 414
QY 115 TyrAspGlyMetSerProGlyProThrPheAsnValProArgGlyThrGluThrValVal 134


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Db      415 TATATGGCATTTACACGAGCCCTACGATCATCGCGAGAGCAAGACCGCTGTA 474
Qy      135 ArphellleasnaalathrValGluasnservalHisleuHisGlySerProserArg 154
Db      475 CGATTCGTAACCAAGGCGATCGCGAGGTCGATTCATCTTCATGGTTCCCTCCGT 534
Qy      155 AlaProheaspGlyTPrpAlaGluaspValThrPheProGly----- 168
Db      535 GCCCCTTTGACGAGTGGCTGAGATTTGAT-TATGAGGGCCCAATTCAAAGGTACAC 593
Qy      169 -----GluTyrLysAspTyr 173
Db      594 AGAACAACTTATGATCAGGGGCTCTTTTATACTAACACAGACTCGTTTATGACTAC 653
Qy      174 TyrPheProAsnTyrGlnSerAlaArgLeuLeuTyrPyrHisAspHisAla----- 190
Db      654 TACTACCGCAACCAAGGCTGCGAGATTCCTGTGTACACAGATCATGCTATGCAATGT 713
Qy      191 -----PheMetLys 193
Db      714 GTAAGCTTGACAGTATATCATGGAGGAGCAAGCAAGATCGGGCTACACTTATGACAG 773
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Qy      214 AspAlaLeuGlyLeuProSerGlyTyrGlyGlnPheAspIleProLeuIleLeuThra 233
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Qy      234 LysTyrTyrAsnAlaAspGlyThrLeuArgSerThrGluGlyGluAspGlnAspLeuTyr 253
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Qy      254 GlyAspValIleHisValAsnGlyGlnProTyrProPheLeuAsnValGlnProArgLys 273
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Qy      294 ThrSerSerProAsnValArgIleProPheGlnValIleAlaSerAspAlaGlyLeuLeu 313
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Qy      334 IleAspPheThrAsnPheAlaGlyGlnThrLeuAsnLeuArgAsnValAlaGluThrAsn 353
Db      1194 TTGCACTTTGGCGCTTATGACGAGGACGATGATTTGGCTAACTTTGCCAAAGGCCAAT 1253
Qy      354 AspValGlyAspGluAspGlyTyrAlaArgThrLeuGluValMetArgPheValSer 373
Db      1254 GGGGTGCGACCGCATGATGATGCAAACTACCAAGGTCAGCGCTCCATGCTCAGC 1313
Qy      374 SerGlyThrValGluAspAsnSerGlnValProSerThrLeuAlaGlyAspValProPhe 393
Db      1314 AGCCACAGCAGTCTGCTGATACCTGGGTACCCGACAGCTATCTCAGATCAGTTCGCC 1373
Qy      394 ProHisLysGlnGlyProAlaAspLysHisPheLysPheGluArgSerAsnGlyHisTyr 413
Db      1374 GCGCACAACACCGCGC---ATGCAACACACACTTCGCTTCATCGCACCAACAGGAGG 1430
Qy      414 LeuIleAsnAspValGlyPheAlaAspValAsnGluArgValLeuAlaLysProGluLeu 433
Db      1431 CGCATCAACGCGATGGGTTTGGACAGGTCGACAAACGATATCTGGCCAAAGGTACCGGC 1490
Qy      434 GlyThrValGluValTPrpGluLeuGluAsnSerSerGlyTyrPsrHisProValHis 453

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Db      1491 GGCATGTGCACTATGGGAACCTCGAGAACAGTCCGGCGGCTGGTGCACCCATCCAC 1550
Qy      454 IleHisLeuValAspPheLysIleLeuLysArgThrGlyGly-----ArgGlyGln 470
Db      1551 GTCCACCTGTGCACTTCGAGTGTGTCGACGCTACAGGTGACGAAGACACTCGCGGC--- 1607
Qy      471 ValMetProTyrGlnSerAlaGlyLeuLysAspValValTPrpLeuGlyArgGlyGluThr 490
Db      1608 GTCAATGCCCTACAGATCGCGCGGTCTCAAGACAGTCGTGTGCTGCGCGCCAGAGACG 1667
Qy      491 LeuThrIleGluAlaHisTyrGlnProTyrPheGlyAlaTyrMetTyrHisCysHisAsn 510
Db      1668 GTGCTGTGCGAAGCAGACTACGCCCCCGGACGAGTCTCAATGTTCCACTGTCCACACAC 1727
Qy      511 LeuIleHisGluAspAsnAspMetLeuAlaValPheAsnValThrAlaMetGluGluLys 530
Db      1728 CTGATCCAGAAACCAAGACATGATGCGCCGCTTGTGAGTACTAAGCTTCAGAACTTT 1787
Qy      531 GlyTyrLeuGln---GluAspPheGluAspProMetAsnProLysTyrPArgAlaValPro 549
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Qy      550 TyrAsnArgAsnAspPheHisAlaArgAlaGlyAsnPheSerAlaGluSerTleThra 569
Db      1848 TTCACCGCGGCTGACTGACGCGCGGATGCTCTTCTGAGAAGCATCATCAGGCT 1907
Qy      570 ArgValGlnGluLeuAlaGluGlnGluProTyrAsnArgLeuAspGluIleLeuGluAsp 589
Db      1908 AGAGTGAACGAGTGGCGCTGGAAACAGCTGACAGCACTGGCAGAGTCAAGGCTCCG 1967
Qy      590 Leu 590
Db      1968 CTC 1970

RESULT 9
US-09-338-723A-3
; Sequence 3, Application US/09338723A
; Patent No. US20020019038A1
; GENERAL INFORMATION:
; APPLICANT: Humming, Wang
; TITLE OF INVENTION: Phenol Oxidizing Enzymes
; FILE REFERENCE: GCS61-2
; CURRENT APPLICATION NUMBER: US/09/338, 723A
; PRIOR FILING DATE: 1999-06-23
; PRIOR APPLICATION NUMBER: 09/220, 871
; PRIOR FILING DATE: 1998-12-23
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 3
; LENGTH: 2905
; TYPE: DNA
; ORGANISM: Bipolaris spicifera
US-09-338-723A-3

Alignment Scores:
Pred. No.: 9.07e-211 Length: 2905
Percent: 1868.00 Matches: 368
Score Similarity: 67.82% Conservative: 81
Best Local Similarity: 55.59% Mismatches: 132
Query Match: 58.58% Gaps: 83
DB: 10 Gaps: 10

US-10-080-233-2 (1-594) x US-09-338-723A-3 (1-2905)
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Db      129 CTCTTCACGACTTCACACTGTTCA-----ATTGCGAAAGGCATATTACGGTGTG 179
Qy      22 ProMetAspThrGlySerHisProIleGluAlaValAspProGluValLysThrGluVal 41
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Qy      42 PheAlaAspSerLeuLeuAlaAlaGlyAspAsp----- 53

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Db      1306  TGTGTGGATTTCGGCGCCCTATGCGCGGCAAAACGTTGGATCTGGGCAAACTCGCAAAAGCC 1365
Oy      352  rAsnAspValGlyAspGluAspGluTyrAlaArgThlLeuGluValMetArgPheValVa 372
Db      1366  CAATGGATCGGTGACCGCGAGCAGCATCGCAAAACATGCACAAAGGTCAATGCTTTCACAGT 1425
Oy      372  1serSerGlyThrValGluAspAsnSerGlnValProSerThrLeuArgAspValProPh 392
Db      1426  CAGCAGCCAAACACTGTCGTCGATTAATCTCCGTCGGTACCCGAGCAGCATATCTCAATCCAGTT 1485
Oy      392  eProProHisIstIuGluProAlaAspLysHisPheLysPheGluArgSerAsnGlyH 412
Db      1486  CCCCCGCGACAAAACC--GACATAGACCAATCACTCCGTTCCATCGTACCAACGCGGA 1542
Oy      412  sTyrLeuIleAsnAspValGlyPheAlaAspValAsnGluArgValLeuAlaLysProG 432
Db      1543  GTGGCGCATCAACGGCATCGGGTTTGCAGACGTGCAGAACCGCTGTTCTGCCAAAGGTACC 1602
Oy      432  uLeuGlyThrValGluValTyrGluLeuGluAsnSerSerGlyLysTyrSerHisProVa 452
Db      1603  GCGGGGTAAGTGTGAGCTTTGGAACTTGAGAACAGCTCCGCGGGGTGGTCAACCCCAT 1662
Oy      452  1His1IleHisLeuValAspPheLysIleLeuLysArgThrLysIleArgGlyGln----- 470
Db      1663  CCAGGTCCACCTAGTACCTTCGAGATCGTCGACGCTACCGGACGACGACGAAGGCACTCGCGG 1722
Oy      471  -ValMetProTyrGluSerAlaGlyLeuLysAspValValTyrLeuGlyArgGlyLysTh 490
Db      1723  CGTATGCGCCATATGAGCGCGCGGTCTCAAGAGACGTGCTGTGGCTCGCGCCCTACAGAAC 1782
Oy      490  rLeuThrIleGluAlaHisIstYrGlnProTyrPthrGlyAlaTyrMetTrpHisCysHisAs 510
Db      1783  GGTCCTCGTCCAAACACATTCACGCCCATGGGAGGTGCATGATGTTCCACTGCCACAA 1842
Oy      510  nLeuIleHisGluAspAsnAspMetMetAlaValPheAsnValThrIleMetGluGly 530
Db      1843  CCTATATCCAGCAACACAGACATGATGCGCGCTTGACGTGACTGAATCAACTCCGAACCTT 1902
Oy      530  sGlyTyrLeuGln--GluAspPheGluAspProMetAsnProLysTrpArgAlaValArg 549
Db      1903  TGGGTACACAGACAGACTGATTCACAGATCTGAGGATCTCGCTGCTGCAGCAAGACC 1962
Oy      549  oTyrAsnArgAsnAspPheHisAlaArgAlaGlyAsnPheSerAlaGluSerIleThrAl 569
Db      1963  TTTTACCGCGGGTATCTCACGGCGCGATCGGGTATCTTTCAAGAAGATCATATCAGAGGC 2022
Oy      569  aArgValGlnIleuAsnIaGluGlnGluProTyrAsnArgLeuAspGluIleLeuGluAs 589
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Oy      589  pLeu 590
Db      2083  GCTC 2086
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US-10-080-210-3
: Sequence 3, Application US/10080210
: Patent No. US200201423A1
: GENERAL INFORMATION:
: APPLICANT: Wang, Huaming
: APPLICANT: Bodie, Elizabeth A.
: TITLE OF INVENTION: Phenol Oxidizing Enzymes
: FILE REFERENCE: GC561-3
: CURRENT APPLICATION NUMBER: US/10/080,210
: CURRENT FILING DATE: 2002-02-19
: PRIOR APPLICATION NUMBER: US 09/220,871
: PRIOR FILING DATE: 1998-12-23
: PRIOR APPLICATION NUMBER: US 09/338,723
: PRIOR FILING DATE: 1999-06-23
: NUMBER OF SEQ ID NOS: 17
: SOFTWARE: FastSeq for Windows Version 4.0
: SEQ ID NO 3
: LENGTH: 2905

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TYPE: DNA
ORGANISM: Bipolaris spicifera
US-10-080-210-3

Alignment Scores:

Pred. No.:	9,07e-211	Length:	2905
Score:	1868.00	Matches:	368
Percent Similarity:	67.82%	Conservative:	81
Best Local Similarity:	55.59%	Mismatches:	132
Query Match:	58.58%	Indels:	83
DB:	12	Gaps:	10

US-10-080-233-2 (1-594) x US-10-080-210-3 (1-2905)

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DB 129 CTCCTCAGCAGCTTCAACTCGTTCA -----ATTGCCAAGGCAATACGGTGC 179
OY 22 PrometaBpThgIySerHisProIleGluAlaValAspProGluValIyThgIuVal 41
DB 180 GCTTTG-----AGCGAAGTCCGCCCAAAATTTGCGACAACACCCCGACGAGAAAG 233
OY 42 PheAlaAspSerLeuAlaAlaIaIaGlyAspAsp----- 53
DB 234 GCTGCC-----TTGGCTCAATTTGTGAACATGACCTCGCGAGTTGTCAACATGCTG 287
OY 54 ---AspTrpGluSerProProTyraIleuLeuTyraGAsnAlaIeuproIleProPro 72
DB 288 AAGACTGCGCAAGCCCGAGATATCTCTCATTTTTCGCAACACACTGCCATCCCTCCA 347
OY 73 ValIyGlnProIyMetIle----- 79
DB 348 GCCAAGGACCAAGTA-GTAGTGTTCATTCGATCGACAGAGTTTCTTGAATATATCTC 406
OY 80 -----IleThraBpRoValThrgIyAspIleTrpTyTrgIuIle 94
DB 407 ACCATCCACAGTAACACTCAGATCTCTCACAAACAGAGATGTGTACTACAGATT 466
OY 95 GluIleIySProPheGlnGlnArgIleTyTrProThleuArgProAlaThleuValGly 114
DB 467 GTCATCAAAACCTTCACCCAGAGTATGATCATGAAGGCGCCGCTCGTTGATAGGC 526
OY 115 TyraSpGlyMetSerProGlyProThrPheAsnValProArgGlyThGluThValVal 134
DB 527 TATGACGCGATCTCCCGAGTCTCAAGTCATAGGCGGAGAGAAAGCAAGCTGTGTA 586
OY 135 ArgPheIleAsnAsnAlaThrValGluAsnSerValHisIleuHisGlySerProSerArg 154
DB 587 CGGTTTAAACCAAGGATGATCGGGAAGCTCCATCTCCACGGCTCCCGCCCGT 646
OY 155 AlaProPheAspGlyTrpAlaGluAspValThrPheProGlyGluTyTrIys----- 171
DB 647 GCCCCTTTTGACGGTGGGTGATGATCATGAAGGGGAATACAA-AGGTACGAT 705
OY 172 -----Asp 172
DB 706 AGCGTGCATCTACGCATCGAAGACCTTATCATTAACAGACATTTTCTTCAGAC 765
OY 173 TyTrTyTrPheProAsnTyGlnSerAlaArgLeuLeuTrpTyHisAspHisAlaPhe-Me 192
DB 766 TACACACCGCAGAAAATGCTATTTTCGGGCAAGCCGCGCCATCTGATCAGACACCGCGC 945
OY 192 t----- 192
DB 826 GTTGTAAAGCTTTTACCGACTTTTCATGTAGTGAACGGAAGATTAGCTAATCATCTGT 885
OY 193 -LysThraIaGluAsnAlaTyrrPheGlyGlnAlaGlyAlaTyrlleIleAsnAspGluAl 212
DB 886 GCAACACCGCAGAAAATGCTATTTTCGGGCAAGCCGCGCCATCTGATCAGACACCGCGC 945
OY 212 aArgValaGlnIleuValIleuProSerGlyTyTrGlyGluPheAspIleProLeuIleuTh 232
DB 946 TGAAGATGCTCTCGGCTTCTCTTCAAGTTACGGAAATATAGACATTCGCGTGTCTCAG 1005
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OY 232 fAlaIyTyTrTyraAsnAlaAspGlyThrLeuArgSerThrGluGluAspGlnAspLe 252
DB 1006 TTCCAGAGTACTACAAACGGCGGATGAGACTCTTAAGACCAAGTGTGGAGAAAGACAGAGTGT 1065
OY 252 uTrpGlyAspValIleHisValAsnGlyGlnProTrpProPheLeuAsnValGlnProAr 272
DB 1066 TTGGGCGCACATCATCCATGTCACAGCGTCAACCCCGCCGCAATTCCTTAATGTGGACCTCG 1125
OY 272 GlyTyTrArgPheArgPheLeuAsnAlaAlaValSerArgAlaTrpLeuLeuTyTrLeuVa 292
DB 1126 AAGATATGCTTTCATTCCTCAACGGCGGCTGTTCCTTAGAAGACTTGGCCCTTACCTTCGT 1185
OY 292 lArgThrSerSerProAsnValArgIleProPheGlnValIleAserAspAlaGlyIle 312
DB 1186 CAAGCAACACAAACACTCGCATAGGCTTCCTTCAGAGTCAATGCTGTGATGACAGGCT 1245
OY 312 uLeuGlnAlaProValGlnThrSerAsnLeuTyTrLeuAlaValAlaGluArgTyTrGluI 332
DB 1246 ACTCACACACCCGGTTCAAACTCAGATATGTATGTTCCACCCCGCAAGACCTACAGAT 1305
OY 332 eIleIleAspPheThraBpPheAlaGlyGlnThleuAspLeuArgAsnValAlaGluTh 352
DB 1306 TGTGTTCATTTTCGCGCCCTATGCGCGCAAAAGTTGATGTGCGCAACTTCGCAAGGC 1365
OY 352 rAsnAspValGlyAspGluAspGluTyTrAlaArgThrLeuGluValMetArgPheValVa 372
DB 1366 CAATGTATCGGTACCGCAGCAGACTACGCAAAACACTGACAGAGTCATGCTTCCACAGT 1425
OY 372 lSerSerGlyThrValGluAspAsnSerGlnValProSerThrLeuArgAspValProPh 392
DB 1426 CAGCAGCAAAACAGTCTGATACCTCGGTGATCCGCAAGACAGTATCTCAGATCAAGTT 1485
OY 392 eProProHisIySglGluGlyProAlaAspIyHisIlePheIySgLeuArgSerAsnGlyH 412
DB 1486 CCGCGGCGCAAAAC--GACATAGACATCACTCTCCGTTTCATGCTTACCAACGGCGA 1542
OY 412 sTyTrLeuIleAsnAspValGlyPheAlaAspValAsnGluArgValLeuAlaIyProGl 432
DB 1543 GTGGGCGCATCAACGCGATCGGTTTGACAGAGTGTGAGAACCGTGTTCGCAAGGTAACC 1602
OY 432 uLeuGlyThrValGluValTrpGluIleuGluAsnSerSerGlyTyTrPheHisProVa 452
DB 1603 GCGCGGTACTGTCAAGCTTTTGGAACTTGAACAGCTCCGCGGCTGTGTACACCCCAT 1662
OY 452 lHisIleHisLeuValAspPheIySleLeuIySArgThrgIyGlyArgGlyGln----- 470
DB 1663 CCAGCTCCACTTAGTACTTCCAGATGCTGCGACCGTACGCGCAAGGCAAGCTCCGCG 1722
OY 471 -ValMetProTyTrGluSerAlaGlyLeuIySAspValAlaTrpLeuGlyArgGlyGluTh 490
DB 1723 CGTATGCGCTTATGAGCGCGCGGCTTCACAGAGCTGTGTGCGCGCTGCACAGAGAC 1782
OY 490 rLeuThrIleGluIleHisTyTrGlnProTrpThGlyAlaIyMetTrpHisCysHisAs 510
DB 1783 GGTCTGTGTGAAACACATTAACGCCCATGAGGAGCGAGCTCAATGTTCACCTCCACAA 1842
OY 510 nLeuIleHisGluAspAsnAspMetAlaValAlaPheAsnValThraIaMetGluGluIy 530
DB 1843 CCTATCCAGCAACACCAAGCATGATGGCGGCTTGACAGTCAATCAACGAGACTT 1902
OY 530 sGlyTyTrLeuGln---GluAspPheGluAspPrometaSnProIyStrpArgAlaValPr 549
DB 1903 TGGGTACACAGACAGACTGATTTCCAGATCTCGAGAGATCTCGGTGCTACAGAACCC 1962
OY 549 oTyraBpArgAsnAspPheHisAlaArgAlaGlyAsnPhSerValaIleuSerIleThraI 569
DB 1963 TTTTCACCGCGGCTATCTCAGCGCGCATGGGATGTTTTCACAAACATTCATCAGCGC 2022
OY 569 aArgValaGlnIleuValaGluGlnIleuProTyTrAspArgLeuAspGluIleuGluAs 589
DB 2023 TAGAGTAAATGATGTGGCGCTTCAGACAGCTTACAGGCAACTCCACAAATGTACAGCTC 2082
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QY	589	pleu	590
		III	
Db	2083	GCTC	2086

Search completed: July 4, 2003, 02:23:25
Job time : 349 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM protein - nucleic search, using frame_plus_p2n model

Run on: July 3, 2003, 22:50:57 ; Search time 2297 Seconds

(without alignments)
4188.123 Million cell updates/sec

Title: US-10-080-233-2

Perfect score: 3189

Sequence: 1 MFKSMQLAASGLSCVLC.....AEQEPYRLELDLIGEE 594

Scoring table:

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Xgapop 10.0, Xgapext 0.5
Ygapop 10.0, Ygapext 0.5
Zgapop 6.0, Zgapext 7.0
Delop 6.0, Delext 7.0

Searched: 16154066 segs, 8097743376 residues

Total number of hits satisfying chosen parameters: 32308132

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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-DB=EST -QMT=fastap -SUFFIX=1st -MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0
-UNITS=bits -START=1 -END=1 -MATRIX=Blasum62 -TRANS=human40.cdi -LIST=45
-DOALIGN=200 -THR_SCORE=ptc -THR_MAX=100 -THR_MIN=0 -ALIGN=10 -MOD=LOCAL
-OUTFMT=ptc -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=200000000
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Database :

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17: gb_gss:*
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22: em_gss_fun:*
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27: em_gss_rtd:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
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2	355.5	11.1	700	10 BE187716	BE187716 BLOX In
3	305.5	9.6	706	10 AW774671	AW774671 EST33822
4	296.5	9.3	848	10 BE216983	BE216983 EST0376 T
5	293.5	9.2	739	10 BO866278	BO866278 OC7113.Y
6	290.5	9.1	592	13 BM143324	BM143324 SE142510
7	283.5	8.9	1128	17 AF094955	AF094955 AF094955
8	277.5	8.7	563	13 BM519618	BM519618 sak81e01
9	256.5	8.0	766	12 BG526127	BG526127 56-88 Ste
10	236	7.4	465	12 BG053739	BG053739 RH12.9.B
11	229.5	7.2	599	12 BF258534	BF258534 HVMET001
12	221	6.9	782	12 BF257494	BF257494 HY_CEA001
13	220	6.9	664	10 BE188099	BE188099 CF377-R
14	212.5	6.7	580	13 BJ159802	BJ159802 BJ159802
15	209	6.6	714	14 BU025469	BU025469 QHF9121.Y
16	208.5	6.5	456	9 A1488265	A1488265 EST246587
17	208	6.5	713	14 BO916926	BO916926 QHB1404.Y
18	208	6.5	717	14 BO971392	BO971392 QHB6M24.Y
19	208	6.5	720	14 BU025741	BU025741 QHG11C24
20	208	6.5	750	14 BO970636	BO970636 QHB42K15
21	205	6.4	786	14 BU025791	BU025791 QHG11H04
22	204	6.4	597	14 BO849512	BO849512 QGB10B15
23	202	6.3	725	14 BO970480	BO970480 QHB42P07
24	201	6.3	725	14 BO970351	BO970351 QHB41M24
25	200.5	6.3	447	17 BH864257	BH864257 SALK_0956
26	196	6.1	693	14 BO965570	BO965570 QHB22E15
27	195	6.1	693	14 BO971750	BO971750 QHB8D22.Y
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31	188	5.9	680	14 BU025091	BU025091 QHF7K04.Y
32	188	5.9	681	14 BO915453	BO915453 QHB14K10
33	188	5.9	690	14 BO915421	BO915421 QHB14118
34	188	5.9	699	14 BO965695	BO965695 QHB22L02
35	187	5.9	726	14 BO971294	BO971294 QHB6H18.Y
36	186	5.8	665	14 BO971648	BO971648 QHB7M11.Y
37	184	5.8	636	14 BU024818	BU024818 QHF6D21.Y
38	184	5.8	645	14 BO965503	BO965503 QHB22B06
39	184	5.8	695	14 BO967332	BO967332 QHB29K19
40	183	5.7	574	14 BO915108	BO915108 QHB13F23
41	183	5.7	630	14 BO914488	BO914488 QHB10L17
42	181	5.7	622	14 BO967966	BO967966 QHB32P19
43	181	5.7	673	14 BO970459	BO970459 QHB42C08
44	181	5.7	681	14 BU023296	BU023296 QHF10G01
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ALIGNMENTS

RESULT 1
LOCUS BE188240
DEFINITION M7ATG In vitro expressed cDNAs Cladosporium fulvum
ACCESSION BE188240
VERSION BE188240.1 GI:8667479
SOURCE Cladosporium fulvum
ORGANISM Cladosporium fulvum
Eukaryota; Fungi; Ascomycota; Pezizomycotina; Dothideomycetes et
Chaetothyriomycetes; Incertae sedis; Mycosphaerellaceae; mitosporic
Mycosphaerellaceae; Cladosporium.
REFERENCE 1 (bases 1 to 600)
AUTHORS Clark,A.J., Rasmussen,S.W. and Oliver,R.P.

TITLE In vitro expressed genes of Cladosporium fulvum
JOURNAL Unpublished (2000)
CONTACT: R.P. Oliver
Necrotrophic Phytopathology Research Centre
Murdoch University
SABC, Perth 6150, Western Australia
Tel: +61-8-9360-7404
Fax: +61-8-9360-6303
Email: roliver@central.murdoch.edu.au
High quality sequence stop: 600
POLYA-No.

FEATURES
source 1..600
/organism="Cladosporium fulvum"
/strain="Race 4"
/db_xref="taxon:5499"
/clone_lib="In vitro expressed cDNAs"
/tissue_type="mycelium"
/note="Vector: Lambda bluescript; A mixture of mycelial cultures grown in liquid B5 for 48 hours and transferred for 24 hours to media lacking carbon, nitrogen or supplemented with hydrogen peroxide"

BASE COUNT 131 a 176 c 162 g 128 t 3 others
ORIGIN

Alignment Scores:

Pred. No.: 1,75e-26 Length: 600
Score: 355.50 Matches: 94
Percent Similarity: 58.33% Conservative: 25
Best Local Similarity: 46.08% Mismatches: 72
Query Match: 11.15% Indels: 15
DB: 10 Gaps: 4

US-10-080-233-2 (1-594) x BE188240 (1-600)

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      |||||
      9 TTCGGGGCCAGATTCTTACTATGNTCAACGGGTCAACAGGGGGCCACAAACACGNGTG 68
OY 355 IGLYSPGLUASPGIUTYTAALARGTHLEUGLVALMETARGPHEVALVAL---SerSe 374
      ::::
      69 NCATACACCGAC-----AAGTCATGAGGCTTCGTCGTTGGAGACAG 110
OY 374 GLYTHRYVALGUASPAASNSERGLVALPROSERTHLEUARGASVALPROPHETOPR 394
      |||
      111 CGTCACCGACAGTCCCAACACACGTCATCACTGACGATGGCGCGGCGGACGCTGTG 170
OY 394 CHISYSGIUGLYPROALASPLYSHISPHELYSPHEGLUARGSERASNGLYHS---Ty 413
      |:::
      171 AGCGCAGGACACATATTGACACACCTTCACTTCCAGATGGCGGCGGCGGACGCTGTG 230
OY 413 TLEULIASNAPVALGLYPHEALASPVASALNSGLUARGVALLEUALALYSPROGLULU 433
      ::::
      231 GACCGTCATAGCGCGTGAATTCAGGACCGCCGACGCGGTGTCGTCGAGCCGACACA 290
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      |||||
      291 AGGCGCTGTCGAGCTGTCGCGCTGACACTGGCGCTCGCGCTGTCACACCGACTACA 350
OY 453 SILEHISLEUVALASPPHELYSILEULYSARGTHRGISYGLYARGISYGLINVALMETPR 473
      |||||
      351 TATCCATCTTGTCAACATGACAGTCTCTCCGCTACTGGTGGTGGCCCGGCTCATATGCC 410
OY 473 OTYGLUSERIALAGLYLEULYSASPVASVALITRPLEUGLYARGISYGLIUTHLEUTHRI 493
      |||||
      411 ATACGACAGCTGCTGTCGAAGAAGAGCTGTATGCTGCTCTGCGACGATGTGACAGCT 470
OY 493 EGLUALAHISTYRGLINPROTTPRTHGLYALATYMETRPHISYSHISASNLEULIHI 513
      :::
      471 GCTTGCTTTTACGCTCTTGGAGAGGCTTGAC-ATGTTTCATTTGCCACAC-CTTGTAACA 528
OY 513 SGLUSPASNASPMETMETALA-VALPHEASNVALTTHALAMETLUGLULYSGLYTYTL 533
      |||||
```

DB 529 CGAAGATCAACCATGATGAGCCCGCTTCAACACGACACCTTGAACCTGGGCTACGAC 588
OY 533 ewuglglu 535
DB 589 TTCACACG 596

RESULT 2
BE187716 700 bp mRNA linear EST 25-SEP-2000
LOCUS BE187716
DEFINITION BILIRUBIN oxidase precursor, mRNA sequence.

ACCESSION BE187716
VERSION BE187716.1 GI:8666955
KEYWORDS EST.

SOURCE Cladosporium fulvum.

ORGANISM Cladosporium fulvum.
Eukaryota; Fungi; Ascomycota; Pezizomycotina; Dothideomycetes et
Chaetothyrionmycetes; Incertae sedis; Mycosphaerellaceae; mitosporic
Myosphaerellaceae; Cladosporium.

REFERENCE 1 (bases 1 to 700)

AUTHORS Clark,A.J., Rasmussen,S.W. and Oliver,R.P.

JOURNAL In vitro expressed genes of Cladosporium fulvum

UNPUBLISHED (2000)

CONTACT: R.P. Oliver

Necrotrophic Phytopathology Research Centre

Murdoch University

SABC, Perth 6150, Western Australia

Tel: +61-8-9360-7404

Fax: +61-8-9360-6303

Email: roliver@central.murdoch.edu.au

High quality sequence stop: 700

POLYA-No.

FEATURES

source

location/Qualifiers

1..700

/organism="Cladosporium fulvum"

/strain="Race 4"

/db_xref="taxon:5499"

/clone_lib="In vitro expressed cDNAs"

/tissue_type="mycelium"

/note="Vector: Lambda bluescript; A mixture of mycelial cultures grown in liquid B5 for 48 hours and transferred for 24 hours to media lacking carbon, nitrogen or supplemented with hydrogen peroxide"

BASE COUNT 158 a 206 c 183 g 146 t 7 others

ORIGIN

Alignment Scores:

Pred. No.: 2,25e-26 Length: 700
Score: 355.50 Matches: 98
Percent Similarity: 58.60% Conservative: 28
Best Local Similarity: 45.58% Mismatches: 74
Query Match: 11.15% Indels: 18
DB: 10 Gaps: 5

US-10-080-233-2 (1-594) x BE187716 (1-700)

```
OY 339 phealaglyglnthleuaspheuarasn-val-----alagluthrasnasya 355
      |||||
      9 TTCGGGGCCAGATTCTTACTATGNTCAACGGGTCAACAGGGGGCCACAAACACGNGTG 68
OY 355 IGLYSPGLUASPGIUTYTAALARGTHLEUGLVALMETARGPHEVALVAL---SerSe 374
      ::::
      69 NCATACACCGAC-----AAGTCATGAGGCTTCGTCGTTGGAGACAG 110
OY 374 GLYTHRYVALGUASPAASNSERGLVALPROSERTHLEUARGASVALPROPHETOPR 394
      |||
      111 CGTCACCGACAGTCCCAACACACGTCATCACTGACGATGGCGGCGGACGCTGTG 170
OY 111 CGTCACCGACAGTCCCAACACACGTCATCACTGACGATGGCGGCGGACGCTGTG 170
OY 394 CHISYSGIUGLYPROALASPLYSHISPHELYSPHEGLUARGSERASNGLYHS---Ty 413
      |:::
      171 AGCGCAGGACACATATTGACACACCTTCACTTCCAGATGGCGGCGGCGGACGCTGTG 230
OY 413 TLEULIASNAPVALGLYPHEALASPVASALNSGLUARGVALLEUALALYSPROGLULU 433
```

Db	Accession	Version	KeyWords	Source	Organism	Reference	Title	Journal	Comment	Features
Db	231	GACCGTCATAGCGCTGGATTTACAGACCCGAACTCGCTGTCTGGCTAGCGCCGACA	290							
Oy	433	UGLThrValGluValITrpGluLeuGluAsnSerSergIylGlyITrPserHisProValH	453							
Db	291	AGGCACGTGCGAGCGTGGCGCCCTCGTGCACACACTGGCGGTCGCTGCCACCCAGTACA	350							
Oy	453	SLIleHisLeuValAspPheLysIleLeuLysISargThylGlyIYargIylGlnValMetP	473							
Db	351	TATCCATCTTGTTCACATGCGAGGCTCTGCGTACGTCGTGTCGCCGTGGCCCTCATGCC	410							
Oy	473	OTyrGluSerAlaGlyLeuLysAspValValITrPLeuGlyYargIylGlnThrLeuITrI	493							
Db	411	ATTCAGACGCTGCTGTCTGTGAAAGCGTCGTTATGCTGTGCTTCGCGACAGTTGCGACGT	470							
Oy	493	GLuAlaHisIstGlyInbProITrPThrIylAlaIYargIylMetITrPHisCysHisAsnLeuIleH	513							
Db	471	GCTTCCTTTACGGCTCTGGACAGCGCTTGAC-ATGTTTCATTCATGCCACAC-CTTGACA	528							
Oy	513	SGluAspAsnAspMetMetAla-ValIheAsnValITrIAlaMetGluGlnLysGlyITrL	533							
Db	529	CGAAGATTCACACCATGTATGGCCCGCGTTCACACAGACACCCCTTGAAAGCTGTGGCTACGAC	588							
Oy	533	eugInGlu-----AspPheGluLysProMetAsnProLys 544								
Db	589	TTCAACAGACACANGCCTTCGC-GAACCAATGATCCGACA 628								
RESULT 3	AM774671									
LOCUS	AM774671	706 bp	mRNA	linear	EST 07-SEP-2000					
DEFINITION	EST333822 KV3 Medicago truncatula cDNA clone pKV3-23H7, mRNA									
ACCESSION	AM774671									
VERSION	AM774671.1	GI:7718588								
KEYWORDS	EST.									
SOURCE	barrel medic.									
ORGANISM	Medicago truncatula									
	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;									
	Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;									
	Rosidae; eustosids I; Fabales; Fabaceae; Papilionoideae; Trifloiae;									
	Medicago.									
REFERENCE	1 (bases 1 to 706)									
AUTHORS	Vandenbosch, K., Hutt, J., Moore, J., Beremand, P., Peng, H., Ellis, L.,									
	Town, C.D., Bowman, C.L., Craven, M.B., Hansen, T.S., Holt, I.E. and									
	Fraser, C.M.									
	ESTs from roots of Medicago truncatula after Rhizobium inoculation									
	Unpublished (1999)									
TITLE	Contact: Vandenbosch K									
JOURNAL	Department of Plant Biology									
COMMENT	University of Minnesota									
	220 Bosel Center, 1445 Gortner Ave, St. Paul, MN 55108, USA									
	Tel: 612 624 2755									
	Fax: 612 625 1738									
	Email: kvandenbosch.umn.edu									
	Texas A&M EST name: MTEBE40TK									
	TIGR sequence name: MTEBE40TK									
	More information is available at:									
	http://chrysis.tamu.edu/medicago									
	Seq primer: Skmod (CTA gaa cta gta gat cc).									
FEATURES	Location/Qualifiers									
Source	1..706									
	/organism="Medicago truncatula"									
	/cultivar="genotype A17"									
	/db_xref="taxon:3880"									

		Stratagene and packaged using GigaPack III Gold packaging extracts. Plasmids containing cDNA inserts were excised from the recombinant lambda-zap phage using Ex-assist helper phage and propagated in XL049 cells."	
BASE COUNT	203 a 154 c 138 g 211 t		
ORIGIN			
Alignment Scores:			
Pred. No.:	3.51e-21	Length:	706
Score:	305.50	Matches:	83
Percent Similarity:	46.91%	Conservative:	31
Best Local Similarity:	34.16%	Mismatches:	84
Query Match:	9.58%	Indels:	45
DB:	10	Gaps:	9
US-10-080-233-2 (1-594) x AW774671 (1-706)			
OY	146 ValHisLeuHISGlySerProSerArgAlaIleProPheAspGly-----	159	
Db	14 GTTCATCTCCACGGGTGAGATTCATGAACCCGAAAGCGATGGTAACCAACTATTTTTC	73	
OY	160 -----TrrAlaGluAspValThrPheProGlyGlu	169	
Db	74 ACCGCTGGATTCAAAATCAAGGACGCCACTTGGACAAA-----	112	
OY	170 TyrIlyAspPyrTyrPheProAsnTyrGlnSerAlaArgLeuTrrPyrGlnHisAspHis	189	
Db	113 ---AAGTCATCTACTATCCAAATTAATCAACACCTGGAAATTTATGGTACCAAGACCAT	169	
OY	190 AlaPheMetLysThrAlaGluAspAlaTyrPheGlyGlnAlaGlyAlaTyrIleIleAsn	209	
Db	170 GCTATGGGTTTGACCAAGTCACCTCTAGCTGGCTTAATTTGGACCTACATCATTCGT	229	
OY	210 AspGluAla---GluAspAlaLeuGlyLeuProSerGlyTyrGlyGluPheAspIlePro	228	
Db	230 GACCTTCGATCGAATCAACACTAAATTTACCAACAGCT---AACGAATTGCATTTACCG	286	
OY	229 LeuIleLeuThrAlaTyrTyrTyrAsnAlaAspIlyThr-----LeuArgSerThrGlu	246	
Db	287 TTGATGTATTCGATCGTAGCTTTAAACGAGCGGTTCGATTTTCATGAACCTCAACTGCT	346	
OY	247 GlyGlu-----AspGlnAspLeuTrrGlyAspValIleHisVal	259	
Db	347 AACAAACCTTCAGATTATCCACAGTGGCAACCGGAATATTTGGTGGACGAATCATTTGTA	406	
OY	260 AsnGlyGlnProTrrProPheLeuAsnValGlnProArgLysTyrArgPheArgPheLeu	279	
Db	407 AACGGTAAAGCTTGCCACGTTTAACGTACAGAGCTGTAAGTATGATTTTCGATCTTC	466	
OY	280 AsnAlaAlaValSerArgAlaTrrPheLeuLeuTyrIleuValArgThrSerSerProAsnVal	299	
Db	467 AATCAAGTAACGCTAGATTTTTTCAGGCTCTTTTC-----AGTAATGGTTTA	514	
OY	300 ArgIleProPheGlnValIleAlaSerAspAlaGlyLeuGlnAlaProValGlnThr	319	
Db	515 AGA-----TTTGTACACGTTGGCATTCGATTCCTATATAGCGGAAGCCGTTTACGAGT	568	
OY	320 SerAsnLeuTrrLeuAlaValAlaGluArgGlyGluIleIleIleAspPheThrAsnPhe	339	
Db	569 AATTAACCTTTGGGGCCATCTGAGATTCACAGATGTATTTGTTGATTTTTCGAATCT	628	
OY	340 AlaGlyGlnThrLeuAspAlaGluArgAsnValAla-----GluTrrAsnAspVal	355	
Db	629 AAGGTAACGTTGCTATTTCTACAGTAATGATGATGCACACTTATCTTACCAACCGGATGCA	688	
OY	356 GlyAspGlu	358	
Db	689 GTTGATGAA	697	
RESULT 4			
LOCUS	BE216983	848 bp	mRNA linear EST 03-JUL-2000
DEFINITION	EST03036 Triticum aestivum lambda-zap Triticum aestivum cDNA clone		

accession JAI_5A_A06_T3 5', mRNA sequence.
 version BE216983
 keywords BE216983.1 GI:8904523
 source EST.
 organism bread wheat.
 Triticum aestivum
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Poidea
 ; Triticeae; Triticum.
 1 (bases 1 to 848)
 reference Anderson, J.M., Williams, C.E. and Goodwin, S.B.
 title Analysis of an EST database reveals a probable CF2 resistance gene
 journal unpublished (2000)
 comment Contact: Anderson, J.M.

High quality sequence stop: 848	FEATURES
Location/Qualifiers	source
1. .848	

```

/clone.lib="Trifolium aestivum lambda zap
/tissue_type="leaf"
/dev_stage="9 day old seedlings"
139 a 312 c 263 g 134 t
BASE COUNT
ORIGIN
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Alignment Scores:	
Pred. No.:	4, 05e-20
Score:	296.50
Percent Similarity:	50.00%
Best Local Similarity:	36.73%
Query Match:	9.30%
DB:	10
Length:	844
Matches:	30
Conservative:	83
Mismatches:	88
Indels:	25
Gaps:	7

US-10-080-233-2 (1-594) x BE216983 (1-848)

QY 173 TyTTyTgRPhneProasNTyGtInSerAlaArgLeuleTrTyThIsaBnHIsAlaPheMet 19

Db 20 TAcAGAGTAACCGAACCAGCAGCCCTCCGGTAACCTGTGGTACCAAGAACGCCATGGGC 79

193 LysThrAlaGluAsnAlaTyrPheGlyGlnAlaGlyAlaTyrIleLeuSnpCgluAa 217
||| ||| ||| |||||||| :::: ||| |||
80 CTCACCCGGTCACATCCTCGCTGCCCTCCTCGGGCGGTACCAGTGTCGCCGACCCGGCA 136

213 GIuaspala---LeuGlyLeuProSerGlyTyrGlyGluPheaspIleProLeuIleLeu 231

140 GCGAGGCGCCCTCGGCTCCCTCCGGC--GCGAGTTCGACCGGACCTCGTCTC 190

[illegible]

2000

[illegible]

263 ProTrpProPheLeuAsnValGlnProArqLysTVrArqpPheArqpPheLeuAsnAlaAla 282

Db 317 GCCTGGCCCTTCTCGCGGTGCGGCGCGCGGTACCGCTTCCGCATCCTCAAGCCAGC 376

QY 283 ValSerArgAlaTrpLeuLeuTyrLeuValArgThrSerSerProAsnValArgIlePro 302

0 / AACGCGGCACACCCGCGC-----TCCGGCGGCCCTCCGC----- 418

OY	30	PhgIInValIAlSerSpaIaGlyLeuEugIInAlProValGInThSerAnLeu	322
		: : : :	
Db	419	TTGCTGCACAGTGGGCTCCGACCTCCGTACTCGCGCGCGCGCTTGCCACGAGGGTTC	478
OY	323	TyrLeuAlaValAlaGluArgTyrGluIleIleIleAspPheThrAsnPheAlaGlyIa	342
		: : : :	
Db	479	TTGCTGCGCCCTCGGAGATCGCGGATGTTCATCGACTTCGCGGGGGCCACAGCACAC	538
OY	343	ThrLeuAspLeuArgAsnValAlaGluThrAsnAspValGlyAspGluAspGluTyrAla	362
		: : : :	
Db	539	GCGGTATCCCTGCGGTCCGACGCGCGCGCGCGCGGACCGCGACCGCGGACGAGAGGG	598
OY	363	ArgThrLeuGluValMetArgPheValAlaSerSerGlyThrValGluAspAsnSerGln	382
		: : : :	
Db	599	GATACGGGGCGCTGATGAAATCGGGGGCGGAGTAC-----	637
OY	383	ValProSerThrLeuArg	388
		: : : :	
Db	638	---CGGACACGACCGG	652

RESULT 5
BQ866278

LOCUS	BQ866278	739 bp	mRNA	linear	EST 14-AUG-200
DEFINITION	GGC7113.yg.ab1 QG_ABCD1 lettuce salinas Lactuca sativa cDNA clone				

ACCESSION	Q6C113, mRNA sequence.
VERSION	B0866278
VERSION	B0866278 1
VERSION	GT..2251743

FUNCTION	GR12222173
KEYWORDS	00002/0.1
SOURCE	EST.
	<i>Lactuca sativa.</i>

ORGANISM *Lactuca sativa*
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Asteridae II; Asterales; Asteraceae; Lactuceae; Lactuca

REFERENCE
AUTHORS
1 (bases 1 to 739)
Lactuca.
Kozik, A., Michelmore, R.W., Knapp, S., Matvienko, M., Rieseberg, L.

Lin, H., van Damme, M., Lavelle, D., Chevalier, P., Ziegler, J., Ellison, P., Kolkman, J., Slabaugh, M. S., Livingston, K., Zhou, Y., Lai, Z.,

TITLE Church, S., Jackson, L. and Bradford, K.
Lettuce and Sunflower ESTs from the Compositae Genome Project
<http://compositae.ucdavis.edu/>

JOURNAL
COMMENT
Unpublished (2002)
Contact: Alexander Kozicki (R.W.Miche)more]
http://compgeom.ics.ucaavis.edu/

Department of Vegetable Crops, R.W. Michelmore Lab
University of California at Davis (UCD)

Asmundson Hall, UCD, Davis, CA 95616, USA
Tel: 1-(530)-742-1742

Fax: 1-(530)-752-9659
 Email: akozik@atgc.org [michelm@vegmall.ucdavis.edu]
 belongs to contic OG CA contic7503 see http://commb.ucdavis.edu/

for details. `row: 1 column: 13.`
 Plate: 06C7 `row: 1 column: 13.`
 details to contact vc@cn.columbia.edu, see <http://cgsb.columbia.edu>

FEATURES	Location/Qualifiers
source	1. .739

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/organism="Lactuca sativa"  
/cultivar="Salinas"
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/db_xref="taxon:4236"
/clone="QGCT113"
/clone_1b="OGC11bcttucc gattucca"

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/cvms_eid=V0_mdb1 recube sarinas
/lab_host="E.coll"
/notes=Vector: DBRCDNASfAB: The 1library was constructed

```

from 10 different sources of RNA from a single genotype. Separate cDNAs were generated using primers that

incorporated unique 5' and 3' tags to distinguish each source of RNA. cDNAs were then pooled, size-fractionated,

directionally cloned into a custom medium-copy vector and transformations made with four size classes to minimize size bias. Details of each source of RNA and library

size diam. Details of each source of RNA and library construction can be obtained at http://cgpub.ucdavis.edu/TAG_LIR-06/ABCDI/lettuce_salinas

```

TAG_TISSUE=chemical induction
TAG_SEQ=TGAGCCGGG"

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BASE COUNT	204 a	167 c	163 g	203 t	2 others
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Db 110 ATGGGCTGACCCGAGTCAACCTTCTAGCTGGCTACTCGAGCCTACATCATTCGCCAC 169
QY 210 ASpgluAlaGluAspAlaLeuGlyLeuProSerGlyTyrGlyGluPheAspIleProLeu 229
Db 170 CCTCAGATCGAGGACCGCTAGGCTTACCCAGCGT---GAGGATTCGATCGAAGCGTG 226
QY 230 IleLeuThrAlaValSerTyrTyrAsnAlaAspGlyThrLeu---ArgSerThrGluGly 248
Db 227 ATCGGTTCGATCGAGCTCCGACAGCGGTTCGATTCATCATGATTCACCGCGAAC 286
QY 249 ASP-----GlnAspLeuTyrGlyAspValIleHisValAsn 260
Db 287 AACCTAAATACACCTTCATGCGACGACGAGATCTTCGGGACGCCATCTGTCAC 346
QY 261 GlyGlnProTyrProPheLeuAsnValGlnProArgLysTyrArgPheArgPheLeuAsn 280
Db 347 GCGAAGGCGTGCGCGCTCATCGGTGGAGCTGATGATCATGATTCGCGATATCAAC 406
QY 281 AlaAlaValSerArgAlaTyrLeuLeuTyrLeuValArgThrSerSerProAsnValArg 300
Db 407 GCCACACAGCGGAGCTTCTAGATTCCTTCCACCAAC-----GGC 448
QY 301 IleProGlnValIleAlaSerAspAlaGlyLeuGlnAlaProValGlnThrSer 320
Db 449 TTGAGATTCACCCACGCTGCGATCCGATTCGCTTACATCGAAGCCGCTCATTCGCAAT 508
QY 321 AsnLeuTyrLeuAlaValAlaGluArgTyrGluIleIleLeuAspPheThrAsnPheAla 340
Db 509 GAGACGCTGCTGGGCGCATCGATGACAGACATCGTTGACTTTTCACATCCAG 568
QY 341 GlyGlnThrLeuAspLeuArgAsn 348
Db 569 AGTAACTTGCTGCTATTCAGCCAC 592

RESULT 7
AF094955/c 1128 bp DNA linear GSS 29- AUG-2000
LOCUS AF094955 Salmonella typhimurium LT2, Lambda DASH II Salmonella
DEFINITION typhimurium genomic clone 74-r73, DNA sequence.
ACCESSION AF094955
VERSION AF094955.1 GI:4322797
KEYWORDS GSS.
SOURCE Salmonella typhimurium.
ORGANISM Salmonella typhimurium.
REFERENCE 1 (bases 1 to 1128)
AUTHORS Wong, R.M.Y. and McClelland, M.
TITLE End Sequences of Salmonella typhimurium LT2 Lambda DASHII Clones,
Li-Cor
JOURNAL Unpublished (1999)
CONTACT: McClelland M
Molecular Biology
Sidney Kimmel Cancer Center
3099 Science Park Road, San Diego, CA 92121, USA
Email: mclelland@lifesci.sdsu.edu
Class: shotgun.
FEATURES
source Location/Qualifiers
1..1128
/organism="Salmonella typhimurium"
/strain="LT2"
/db_xref="taxon:602"
/clone="74-r73"
/clone_lib="Salmonella typhimurium LT2, Lambda DASH II"
/note="Vector: Lambda DASH II; sequenced using Li-Cor
sequencer"

BASE COUNT 260 a 352 c 305 g 211 t
ORIGIN

Alignment Scores: 1.44e-18 Length: 1128
Pred. No.: 283 50 Matches: 96
Percent Similarity: 38.72% Conservative: 43

Best Local Similarity: 26.74% Mismatches: 127
Query Match: 8.89% Indels: 93
DB: 17 Gaps: 9
US-10-080-233-2 (1-594) x AF094955 (1-1128)

QY 1 MetLeuPheLysSerTyrGlnLeuAlaAlaSerGlyLeuLeuSerGlyValLeuGly 20
Db 1066 ATGATTCACGTCGCGCTGATTCCTTCAGCATGCG-----GGA 1028
QY 21 IleProMetAspThrGlySerHisProIleGlnAlaValAspProGlnValLysThrGlu 40
Db 1027 ATCCGATATGTCAGCGCGCATTCCTCTCAGGCG----- 992
QY 41 ValPheAlaAspSerLeuLeuAlaAlaGlyAspAspAspTyrGlyLysSerProTyr 60
Db 991 -----AATCTCCCGGTGAG----- 977
QY 61 AsnLeuLeuTyrArgAsnAlaLeuProIleProProValLysGlnProLysMetIleIle 80
Db 976 -----CAACACCGCTGCTGCTCCGCGCTGCGAGTCCGCGC----- 935
QY 81 ThrAsnProValThrGlyLysAspIleTyrTyrGluIleGluIleLysProPheGln 100
Db 934 -----GGG 932
QY 101 GlnArgIleTyrProThrLeuArg-----ProAla 110
Db 931 CAGCGGTGTTTATGACGCTACAGGACGCGAGCTGCTTACGCAAGGACGCGCGCG 872
QY 111 ThrLeuValGlyTyrAspGlyMetSerProGlyProThrPheAsnValProArgGlyThr 130
Db 871 CCGGCTCGGAGATGACAGCGTCGTATCTGGGGCGGCAATCCGCGCTGGAAAGCGCAT 812
QY 131 GluThrValValArgPheIleAsnAsnAlaThrValGluAsnSerVal----- 146
Db 811 GACGTTAATCATCATATAGCAACCGCCTGGCGGAAATGCTCTCATACGCTGCTGCT 752
QY 147 -----HisLeuHisGlySerProSerArg-----AlaProPheAspGly 159
Db 751 TTACTGTCGCGGGCGCGCTGATGGTGCGCGGCGGTATGATGTCGCGAAGCGGAC 692
QY 160 TrrAlaGluAspValThrPheProGlyLysIleTyrLysAspTyrTyrPheProAsnTyrGln 179
Db 691 TGGGCGCGC-----GCTTTCGCCATTCGTCAG 665
QY 180 SerAlaArgLeuLeuTyrTyrHisAspHisAlaPheMetLysThrAlaGluAsnAlaTyr 199
Db 664 AGCGCGCGGACGCTGTGTATCAGCTAACACGCTTAACCGCAGCGCGACAGGTAT 605
QY 200 PheGlyGlnAlaGlyAlaTyrIleLeuAsnAspGluAlaGluAspAlaLeuGlyLeuPro 219
Db 604 AACGCGCGGACGAGATGTGGCTGTGTCAGACGATCAATAAACGCTGCCATTCGCG 545
QY 220 SerGlyTyrGlyGluPheAspIleProLeuIleLeuThrAlaValTyrTyrAsnAlaAsp 239
Db 544 AACCATTCAGCGCGATGATTTCCCTCATATCCAGATTAACCGCGCTGATTAACCTT 485
QY 240 GlyThrLeuArgSerThrGluGlyLysAspLysPheLeuTyrGlyAspValIleHisVal 259
Db 484 GGGAGCGCGGAGTACAGGAAACCGGAGCGGTGTTGTCGCGCATACCTGCTGTG 425
QY 260 AsnGlyGlnProTyrProPheLeuAsnValGlnProArgLysTyrArgPheArgPheLeu 279
Db 424 AACGGCGCGCAAGCCCTATATGTCGAGTTCGCGCGCTGCGGTTCAGTTCGTTG 365
QY 280 AsnAlaAlaValSerArgAlaTyrLeuLeuTyrLeuValArgThrSerSerProAsnVal 299
Db 364 AACGCTCGAATCGCGCGCTATCAGCTTCAGATGAGCATGCGATGCGCGCGC----- 314
QY 300 ArgIleProPheGlnValIleAlaSerAspAlaGlyLeuGlnAlaProValGlnThr 319
Db 313 -----CTGCATGTGATTCAGCGCATCAGGCGCTTTTAACTGCGCGGCTTCGCTC 263

Oy		320 SerasnuenyrluaAlavalAalAGlunkrgrYgrrgllelleilleilaePheThrasn 338 : :
Dd	262 AAACNGTGTCTACTGGCCCGGCGCAGCACTGAATTCGTGTTGATTATGCACAAC 206	
RESULT 8	BMS19618	563 bp mRNA linear EST 15-FEB-2002
LOCUS	sra81801.y1 Gm-cl036 glycine max cdna clone SOYBEAN CLONE ID: Gm-cl036-9433 5' similar to TR:O23123 O23123 F19GI0.5 PROTEIN. ;,	
DEFINITION	mRNA sequence.	
ACCESSION	BMS19618	
VERSION	BMS19618.1 GI:18690770	
KEYWORDS	EST.	
SOURCE	soybean. glycine max	
ORGANISM	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae; Glycine.	
REFERENCE	1 (bases 1 to 563) Shoemaker,R., Kelm,P., Vodkin,L., Espelding,J., Coryell,V., Khanna, A., Bolla,B., Maitra,M., Hillier,L., Knutaba,T., Martin,D., Beck,C., Wylie,T., Underwood,K., Steptoe,M., Theising,B., Allen,M., Bowers, Y., Person,B., Swaller,T., Gibbons,M., Pape,D., Harey,N., Schurk, R., Ritter,E., Korn,S., Shin,T., Jackson,Y., Cardenas,M., McCann, R., Waterston.R. and Wilson,R. Public Soybean EST Project Unpublished (1999)	
TITLE	Contact: Shoemaker R/Public Soybean EST Project	
JOURNAL	Public Soybean EST project	
COMMENT	Washington University School of Medicine 444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA Tel.: 314 286 1800 Fax: 314 286 1810 Email: est@wustl.edu This clone is available through: Resgen, Invitrogen Corp. 2130 South Memorial Parkway Huntsville, AL 35801 For further information call: (800)-533-4363 or contact: cuc@resgen.com web site: www.resgen.com Seq primer: -40RP from GlbCO High quality sequence stop: 433. Location/Qualifiers 1..563 /organism="Glycine max" /db_xref="taxon:3847" /clone-"SOYBEAN CLONE ID: Gm-cl036-9433" /_feature_1fb="Gm-cl036" /_tissue_type="somatic embryos cultured on MSD 20" /_lab_host="DHIOB" /note="Vector: pSPORtl; Site1: NotI; Site2: SalI; This cdna library was constructed from mRNA isolated from somatic embryos (age ranging from 2 months to 9 months) cultured on MSD 20. The library was prepared using the Life Technologies superscript cdna library construction kit. Complementary DNA was synthesized from mRNA using a poly (dT) sequence with a NotI restrictions site. SalI linkers adapters were ligated to the blunt-ended CDNA fragments followed by NotI digestion. The cDNA fragments were directionally cloned into the NotI-SalI restriction site of the pSPORT1 vector. The ligated CDNA fragments were transformed into E.coli Electorax DHIOB host cells. This library was constructed in the laboratory of Dr. Lila Vodkin by Anu Khanna at the University of Illinois at Urbana-Champaign. e-mail: l-vodkin@uiuc.edu"	
BASE COUNT	141 a 171 c 128 g 123 t	
ALIGNMENT SCORES:	Pred. No.: 1.95e-18 Length: 563	
Score:	277.50 Matches: 67	
Percent Similarity:	53.72% Conservative: 34	
Best Local Similarity:	35.64% Mismatched: 70	

Query Match:	8.70%	Indels:	17
DB:	13	Gaps:	5
US-10-080-233-2 (1-594) x BM519618 (1-563)			
QY	174 TyrPheProAsnTyrGlnSerAlaArgLeuLeuTrrTyrHisAspHisAlaPheMetLys	193	
Db	3 CACTACCCAAATATATCAACCAACCGGGAAACCTATGTATGCATGACCATGCGCATGGGGTTG	62	
QY	194 ThrAlaGluAsnAlaTatTyrPheGlyGlnAlaGlyAlaTrrIleIle---AsnAspGluAla	212	
Db	63 ACCCGAGTCACCTTCTAGCTGGCTACTCGAGGCTTACATCATTCATTCGCCACCTTAGATC	122	
QY	213 GluAspAlaLeuGlyLeuProSerGlyTyrGlyGluPheAspIleProLeuIleLeuThr	232	
Db	123 GAGACACCCCGTAGGCTTATCCACGGGT---GACAAATTCGATCGAAGCTGATCGTTC	179	
QY	233 AlaLysTyrTyrAsnAlaAspGlyThrLeu---ArgSerThrGluGlyGluAsp-----	249	
Db	180 GATGCGAGCTTCCCGACGGAGCGGTTCGATCTTCATGAGCTTCACCGCGGACACACCTTAA	239	
QY	250 -----GlnAspLeuTrpGlyAspValIleHisValAsnGlyGlnPro	263	
Db	240 ATTACACCTCAGTGGCAGCCAGAGTACTTCGGCGACGCCCATTCATTGTATACGGCAAGCG	299	
QY	264 TrpProPheLeuAsnValGlnProArgLysTyrArgPheArgPheLeuAsnAlaAlaVal	283	
Db	300 TGGCCGGCGGCTACAGTCCGACGCGCGTAAATGATGATTCGCGATTAATCAAGCCAGCAAC	359	
QY	284 SerArgAlaTrpLeuLeuTyrLeuValArgThrSerSerProAsnValArgIleProPhe	303	
Db	360 GCCAGGGTCTTTCATATCTTCTTCACCAAC-----GGCTTGAGATTTC	401	
QY	304 GlnAlaIleAlaSerAspAlaGlyLeuLeuGlnAlaAlaProValGlnThrSerAsnLeuTyr	323	
Db	402 ACCCAGCGGATCGCATTCGCGTTACTATCGAGAAGCCGTAAGACCAATGAGACGGCTG	461	
QY	324 LeuAlaValAlaGluArgTyrGluIleIleIleAspPheThrAsnPheAlaGlyGlnThr	343	
Db	462 GTGGGGCCATTTGGATCATCCAGACATCGTTGTTCATTCATTCACAGAGTAACCTTG	521	
QY	344 LeuAspLeuArgAsnValAlaGlu	351	
Db	522 GCTATTCTAGCCACGATGCATAA	545	
RESULT 9			
BG526127			
LOCUS	56-88	Stevia field grown leaf cDNA	Stevia rebaudiana cDNA 5', mRNA
DEFINITION			
ACCESSION	BG526127		
VERSION	BG526127.1	GI:16949596	
KEYWORDS	EST.		
SOURCE	Stevia rebaudiana.		
ORGANISM	Eukaryotes; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Asteridae; euasterids II; Asterales; Asterales; Asterales; Asteroideae; Helianthaceae; Stevia.		
REFERENCE	1 (bases 1 to 766)		
AUTHORS	Brandle,J.E., Richman,A., Swanson,A.K. and Chapman,B.P.		
TITLE	Leaf ESTs from Stevia rebaudiana: A resource for gene discovery in diterpene synthesis		
JOURNAL	Unpublished (2001)		
COMMENT	Contact: Jim Brandle Genomics and Biotechnology Agriculture and Agri-Food Canada - SCPPFC 1391 Sandford St., London, Ontario, CANADA, N5V 4T3 Tel: 519 457 1470 Fax: 519 457 3997 Email: brandleje@em.agr.ca Seq primer: T3 promoter primer. Location/Qualifiers		
FEATURES			


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QY 212 AlaglnAspAlaLeuGlyLeuProSerGlyTyrGlyGlnPheAspIleProLeuIleLeu 231
   :::: :::: ||||| :::: :::: ||::: ||:::
Db 332 GTGACGCTCCCGATGATCTTCCCTGC-----GACGACGACGACCTCCACCTGTCGTC 279
QY 232 ThrAlaLysTyrTyrAsnAlaAspGlyThrLeu--ArgSerThrGlnGlyGlu----- 248
   :::: :::: ||||| ::::: |||
Db 278 GCGGACCGCAGCTTCAACGTCGACGCTCGCTGACATGAATCCACGCGGCTGCGCCG 219
QY 249 -----AspGlnAspLeuTrpGlyAspValIleHisValAsnGlyGln 262
   :::: :::: ||::: :::: ||||| ::::
Db 218 TCCGTCACCCACAGTGGCAGCCCGAGTACTTCGCTGAGCGCCGTCACCGTCACGCGCAG 159
QY 263 ProTrpProPheLeuAsnValGlnProArgLysTyrArgPheArgPheLeuAsnAlaAla 282
   ||||| ||| ::::: ||||| ||||| ::::
Db 158 GCGTGGCCGTTCTCCGCCGTCACCGCGGCGTACCGCTTCGCGATCTCAACGCCAGC 99
283 ValSerArgAlaTrpLeuLeuTyrLeuValArgThrSerSerProAsnValArgIlePro 302
   ::||| :::: |||
98 ACGCGCGCTACTTCAACGTCCTCGCTC-----TCCAACGGCATGCCC 57
QY 303 PheGlnValIleAlaSerAspAlaGlyLeuLeuGlnAlaProVal 317
   ||| ||::: ||||| ||| ||||| |||
Db 56 TTCACACGTCGTCGCTCGACGCGTCGTCACCTCGCCGCGCGGTC 12
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Job time : 2310 secs

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